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OM nucleic - nucleic search, using sw model
Run on: March 23, 2005, 02:08:08 ; Search time 520 Seconds
(without alignments)
14173.227 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
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3: Geneseqn2000s:*
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10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1245	100.0	3786	10 AAD62305	Aad62305 Candida a
2	1046.6	84.1	3813	10 AAD62309	Aad62309 Candida a
3	949	76.2	4383	10 AAD62312	Aad62312 Candida a
4	947.4	76.1	3360	10 AAD62307	Aad62307 Candida a
5	895	71.9	1404	10 AAD62306	Aad62306 Candida a
6	733.4	58.9	1407	10 AAD62308	Aad62308 Candida a
7	713.8	57.3	1404	10 AAD62313	Aad62313 Candida a
8	574.6	46.2	4332	10 AAD62310	Aad62310 Candida a
9	393.6	31.6	6897	10 AAD62311	Aad62311 Candida a
C 10	82.4	6.6	100	2 AAQ62588	AAQ62588 Candida a
C 11	82.4	6.6	100	2 AAQ62590	AAQ62590 Candida a
C 12	76	6.1	100	2 AAQ62589	AAQ62589 Candida a
C 13	68	5.5	100	2 AAQ62592	AAQ62592 Candida a
14	61.4	4.9	5511	3 AA61847	AA61847 Cryptospor
15	61.4	4.9	5511	6 ABT04776	ABT04776 C parvum
16	61.4	4.9	7334	3 AA61846	AA61846 Cryptospor
17	61.4	4.9	7334	6 ABT04775	ABT04775 C parvum
C 18	57.2	4.6	100	2 AAQ62593	AAQ62593 Candida a
C 19	57	4.6	100	2 AAQ62591	AAQ62591 Candida a
C 20	56.4	4.5	204803	12 ADQ97348	Adq97348 Mouse can

21	55.4	4.4	436	4	AAI12933	Aai12933 Probe #28
22	55.4	4.4	436	4	ABA54635	Aba54635 Human foe
23	55.4	4.4	436	4	AAI34296	Aai34296 Probe #29
24	55.4	4.4	436	4	ABA44186	Aba44186 Human bre
25	55.4	4.4	436	4	ABA24419	Aba24419 Probe #28
26	55.4	4.4	436	4	AAK28369	Aak28369 Human bon
27	55.4	4.4	436	4	AAK02925	Aak02925 Human liv
28	55.4	4.4	436	4	ABS27968	Abse27968 Human liv
29	55.4	4.4	436	5	AAI02854	Aai02854 Probe #28
30	55.4	4.4	436	6	ABS02878	Abso2878 Human gen
31	55.2	4.4	5163	2	AAV20700	Aav20700 Cryptospor
32	55.2	4.4	5163	3	AAA61849	Aaa61849 ORF encod
33	55.2	4.4	5163	6	ABT04778	Abt04778 C parvum
34	55.2	4.4	5318	6	AAA61848	Aaa61848 DNA encod
35	55.2	4.4	5318	3	AAI04777	Aai04777 C parvum
36	53.6	4.3	5318	2	AAV20701	Aav20701 Cryptospor
C 37	53.2	4.3	3111	8	ACA40105	Aca40105 Prokaryot
C 38	49.4	4.0	7758	6	ABL33102	Ab133102 Human imm
39	48.8	3.9	110000	12	ADH69807_0	Adh69807 Human vbe
40	48.6	3.9	267156	6	ABL68560	Ab168560 Kidney ca
41	48.6	3.9	424	2	AAT29067	Aat29067 Probe for
C 42	47	3.8	1893	8	ACA28989	Aca28989 Prokaryot
C 43	47	3.8	48551	6	AAS20800	Aas20800 Clostridi
44	45.8	3.7	3567	3	AAA70117	Aaa70117 Plasmodiu
45	45.6	3.7	1830	6	ABL56243	Ab156243 Am8PV met

ALIGNMENTS

RESULT 1
AAD62305
ID AAD62305 standard; DNA; 3786 BP.
XX
AC AAD62305;
XX
DT 15-JAN-2004 (first entry)
XX
DE Candida albicans agglutinin-like sequence (ALS) 1 gene.
XX
KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
XX
KW candidiasis; vaccine; fungicide; gene; ss.
XX
OS Candida albicans.
XX
FH Key Location/Qualifiers
FT CDS I..3783
FT /tag= a
FT /product= "C. albicans ALS protein"
FT /codon= (seq:"ctg", aa:Ser)
XX
XX
PN US2003124134-A1.
XX
PD 03-JUL-2003.
XX
PF 13-SEP-2002; 2002US-00245802.
XX
PR 19-NOV-1999; 99US-0166663P.
XX
PR 18-NOV-2000; 2000US-00715876.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX
XX WPI; 2003-810971/76.
XX
DR P-PSDB; ABW01168.
XX
PT New monoclonal antibody against Candida albicans agglutinin-like sequence
XX
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
XX
PT candidiasis, or to generate an immune response that blocks adherence of
XX
XX the organism.
XX
PS Disclosure; Page 12-14; 65pp; English.

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XX CC The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX SQ Sequence 3786 BP; 1170 A; 899 C; 592 G; 1225 T; 0 U; 0 Other;
Query Match. 100.0%; Score 1245; DB 10; Length 3786;
Best Local Similarity 100.0%; Pred. No. 1.4e-287;
Matches 1245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCAATCACTGGTGTGTTTGTAGTATTTTAAATTCATTAACCTTGGTCCAAATGCTGCTAAT 60
DB 52 AAGCAATCACTGGTGTGTTTGTAGTATTTTAAATTCATTAACCTTGGTCCAAATGCTGCTAAT 111
QY 61 TATGCTTTCAAAGGCCAGGATACCCAACTTGGAACTGCTGTTTGGGTTGCTCCTTAGAT 120
DB 112 TATGCTTTCAAAGGCCAGGATACCCAACTTGGAACTGCTGTTTGGGTTGCTCCTTAGAT 171
QY 121 GGTACCAAGTCCAAATCCAGGGGATACATTCACATTTGAATATGCCATGTGTGTTTAAATAT 180
DB 172 GGTACCAAGTCCAAATCCAGGGGATACATTCACATTTGAATATGCCATGTGTGTTTAAATAT 231
QY 181 ACTACTTCAAACAATCTGTGTTGATTAACTGCCGATGGTGTAAATATGCTACTGTGCAA 240
DB 232 ACTACTTCAAACAATCTGTGTTGATTAACTGCCGATGGTGTAAATATGCTACTGTGCAA 291
QY 241 TTTTATTTCTGGTGAAGAAATTCACAACTTTTTCATTAACATGCTACTGTGAACGAGCT 300
DB 292 TTTTATTTCTGGTGAAGAAATTCACAACTTTTTCATTAACATGCTACTGTGAACGAGCT 351
QY 301 TTGAAATCATCCATTAAGGCAATTTGGTACAGTTACTTTTACCAATTCATTTCAATTTGGT 360
DB 352 TTGAAATCATCCATTAAGGCAATTTGGTACAGTTACTTTTACCAATTCATTTCAATTTGGT 411
QY 361 GGAACAGGTTCACTCACTGATTTGGAAAGATTCCTAAATGTTTACTGCTGGTACCAATACA 420
DB 412 GGAACAGGTTCACTCACTGATTTGGAAAGATTCCTAAATGTTTACTGCTGGTACCAATACA 471
QY 421 GTCACTTTTAATGATGGTGTAAAGATATCTCAATTCATGTTGAGTTTGAAGAGTCAACC 480
DB 472 GTCACTTTTAATGATGGTGTAAAGATATCTCAATTCATGTTGAGTTTGAAGAGTCAACC 531
QY 481 GTTGATCCAGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCACA 540
DB 532 GTTGATCCAGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCACA 591
QY 541 ACTCTTTTGTGGCACCACAAATGGAATAAGTTTACACATCTGGTACAAATGGGGTTCTCC 600
DB 592 ACTCTTTTGTGGCACCACAAATGGAATAAGTTTACACATCTGGTACAAATGGGGTTCTCC 651
QY 601 AGTAGTAACGCTGACGTTGCTATTGATTGCTCAAAATATTCATATTTGTTATCACAAAAGGA 660
DB 652 AGTAGTAACGCTGACGTTGCTATTGATTGCTCAAAATATTCATATTTGTTATCACAAAAGGA 711
QY 661 TTAATGATTTGGAATTTATCCGGTTTCATCTGAAATCATTTAGTTTACACTAAAATCTGTACA 720
DB 712 TTAATGATTTGGAATTTATCCGGTTTCATCTGAAATCATTTAGTTTACACTAAAATCTGTACA 771
QY 721 TCTAATGGAATTCAGATTAATATCAAAATGATCTGCTGTTATCTGCTCAATTTATTTGAT 780
DB 772 TCTAATGGAATTCAGATTAATATCAAAATGATCTGCTGTTATCTGCTCAATTTATTTGAT 831
QY 781 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTATACT 840
DB 832 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTATACT 891
QY 841 TGTGCTGGCAGTCTGCTGCAAAAGTAAACCTTTTCACTTTTAAAGATGGAAGTGGATACAAGAA 900
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DB 892 TGTGCTGGCAGTCTGCTGCAAAAGTAAACCTTTTCACTTTTAAAGATGGACTGGATACAAGAA 951
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DB 952 AGTGATGCCGGATCTAAACGGTATTGTTCATTGTTGCTTACAACTAGAACAGTTTACAGACAGT 1011
QY 961 ACCACTGCTGCTCACTACTTTTACCATTCAATCCAAAGTGTGTGATAAAACCAAAACAAATCGAA 1020
DB 1012 ACCACTGCTGCTCACTACTTTTACCATTCAATCCAAAGTGTGTGATAAAACCAAAACAAATCGAA 1071
QY 1021 ATTTGCAACCTATTTCACACCTACCATCACAACTTCATATGTTGGTGTGACTACTTCC 1080
DB 1072 ATTTGCAACCTATTTCACACCTACCATCACAACTTCATATGTTGGTGTGACTACTTCC 1131
QY 1081 TATCTGACTAAGACTGACCAAAATTTGGTGAACAGCTACTGTTTATTGTTGATGTCATAT 1140
DB 1132 TATCTGACTAAGACTGACCAAAATTTGGTGAACAGCTACTGTTTATTGTTGATGTCATAT 1191
QY 1141 CATACTACCACAACTGTTTACCAGTGAATGGACAGGAAACAAATCACTACCAACCAACTCGT 1200
DB 1192 CATACTACCACAACTGTTTACCAGTGAATGGACAGGAAACAAATCACTACCAACCAACTCGT 1251
QY 1201 ACCAATCCAACTGATTCAATTTGACACAGTGGTGGTACAAAGTTCCA 1245
DB 1252 ACCAATCCAACTGATTCAATTTGACACAGTGGTGGTACAAAGTTCCA 1296

RESULT 2
AAB62309
ID AAB62309 standard; DNA; 3813 BP.
XX AC AAB62309;
XX AC
XX DT 15-JAN-2004 (first entry)
XX DE Candida albicans agglutinin-like sequence (ALS) 5 gene.
XX KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
XX KW candidiasis; vaccine; fungicide; gene; ss.
XX OS Candida albicans.
XX FH Key
XX CDS 1. .3813
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XX FT /product= "C. albicans ALS protein"
XX FT /codon= (seq:"ctg", aa:Ser) /codon= (seq:"ttg", aa:Tyr)
XX US2003124134-A1.
XX PD 03-JUL-2003.
XX PF 13-SEP-2002; 2002US-00245802.
XX PR 19-NOV-1999; 99US-0166663P.
XX PR 18-NOV-2000; 2000US-00715876.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Edwards JB, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX WPI; 2003-810971/76.
XX DR P-PSDB; ABW01172.
XX XX New monoclonal antibody against Candida albicans agglutinin-like sequence
XX PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
XX PT candidiasis, or to generate an immune response that blocks adherence of
XX PT the organism.
XX PS Disclosure; Page 26-27; 65pp; English.
XX CC The present invention relates to a monoclonal antibody against an
```

CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of *Candida*
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is *Candida*
CC albicans agglutinin-like sequence (ALS) gene
XX
SQ

Sequence 3813 BP; 1172 A; 819 C; 641 G; 1181 T; 0 U; 0 Other;

Query Match 84.1%; Score 1046.6; DB 10; Length 3813;
Best Local Similarity 90.0%; Pred. No. 4.1e-240;
Matches 1121; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Qy	1	AAGCAATCACTGGTGTGTTTATGATGTTTAAATCACTGCTCCCAATGCTGCTAAT	60
Db	52	AAGCGGATCACTGGTGTGTTTCAATAGTATGACATTAATGCTGCTCAATGCTGGCAT	111
Qy	61	TATGCTTTCAAGGGCCAGGATACCCAACTTGGAAATGCTGTTTGGGTGGTCTTAGAT	120
Db	112	TACGCTTCAAGGACCAAGGATACCCAACTTGGAAATGCTGTTTGGGTGGTCTTAGAT	171
Qy	121	GGTACAGTGCAATCCAGGGGATACATTCATTAATGCAATGCAATGCTGTTTAAATAT	180
Db	172	GGTACAGTGCAATCCAGGAGATACATTCATTAATTAACATGCCATGCTGTTTAAATTC	231
Qy	181	ACTACTTCAAAACATCTGTTGATTTAACTGCGCATGGTAAATATGCTACTTGTCAA	240
Db	232	ACTGCTTCCCAAAATCTGTTGATTTGACTGCCGATGGTAAATATGCTACTTGTCAA	291
Qy	241	TTTTATTCTGCTGAAGAAATCACAACTTTTCTACATTAACATGTAAGTGAACGACGT	300
Db	292	TTTTATTCTGCTGAAGAGTTTACAACTTTTCTACATTAACATGTAAGTGAACGACGT	351
Qy	301	TTGAAATCAATCAATTAAGGCATTTGGTACAGTACTTTTACCAATGCAATCAATGTTGGT	360
Db	352	TTGAAATCAATCAATTAAGGCATTTGGTACAGTACTTTTACCAATGCAATCAATGTTGGT	411
Qy	361	GGACAGGTTCAATCAATGTTGGAAGATCTAAATGTTTACTGCTGGTACCAATACA	420
Db	412	GGACAGGTTCAATCAATGTTGGAAGATCTAAATGTTTACTGCTGGTACCAATACA	471
Qy	421	GTCATATTATGATGGTGAATAAGATATCTCAATTTGATGTTGAGTTTGAAGTCAACC	480
Db	472	GTAACATTTATGATGGCAGTAAAGAGTCTCAATGCTGTTTAAATTTGAAGTCAACA	531
Qy	481	GTTGATCCAGTGCCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATTAAGTCA	540
Db	532	GTTGATCCAGTGCCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATTAAGTCT	591
Qy	541	ACTCTTTTGGGACCAATGTAAGTGAATAATGTTTACATCTGTTACCAATGGGTTCTCC	600
Db	592	ACTCTTTTGGGACCAATGTAAGTGAATAATGTTTACATCTGTTACCAATGGGTTCTCC	651
Qy	601	AGTACTAAGGTGAGTGTGCTATTGATGCTCAAAATATTATGTTGTTATCACAAAGGA	660
Db	652	ACTAGTTAAGGATGTTGCTATTGATGCTCAAAATATTATGTTGTTATCACAAAGGA	711
Qy	661	TTAAATGATGGAATTAATCCGGTTTCATCTGAATCAATTTAGTACACTAAAATTTGAT	720
Db	712	GTAATGATGGAATTAATCCAGTTTACGTTCAATCAATTTAGTACACTAAAATTTGAT	771
Qy	721	TCTAATGGAATTAATCAAAATGTAAGTGAATAATGTTTACATCTGTTACCAATTTTAT	780
Db	772	TCTTTTGGTATCTCTATCACATATCAAAATGTTCTGCGGGTATCGTCCATTTATTCAC	831
Qy	781	GCTTATATTCTGCTACAGATGTTAAACCAATATCTTTAGCATATACCAATGATTTACT	840
Db	832	GCTTATATTCTCTCCCTCAGATTAATCAAGTATCAATTTGCTGATAAAATGACTATACT	891
Qy	841	TGTGCTGGCAGTGTGCTGCAAGTAAACCTTTTCACTTTAAGATGCACTGGATACAAGAT	900
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Qy	901	AGTGATGCCGGATCTAACGGTATTTGTCATTTGTTGCTACAACTAGAACAGTTACAGACGT	960
Db	952	AGTGATGCCGGATCTAACGGTATTTGTCATTTGTTGCTACAACTAGAACAGTTACAGACGT	1011
Qy	961	ACCAGTCTGCTGCTACTTACCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT	1020
Db	1012	ACCAGTCTGCTGCTACTTACCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT	1071
Qy	1021	ATTTTGCAACTATTTCCAACTTACCATTCATTCATTCATTCATTCATTCATTCATTCAT	1080
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Db	1132	TATCTGATTAAGTCTGACCAATTTGGTGAACAGCTACTGTTATTTGTTGATGCTGCTAT	1191
Qy	1141	CATCTACCACTGTTTACCACTGTTGATGCAAGTGAACAGCTACTGTTATTTGTTGATGCT	1200
Db	1192	CATCTACCACTGTTTACCACTGTTGATGCAAGTGAACAGCTACTGTTATTTGTTGATGCT	1251
Qy	1201	ACCAATCCAACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT	1245
Db	1252	ACCAATCCAACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT	1296

RESULT 3
AAD62312
ID AAD62312 standard; DNA; 4383 BP.
XX
AC AAD62312;
XX
DT 15-JAN-2004 (first entry)
XX
DE *Candida albicans* agglutinin-like sequence (ALS) 8 gene.
XX
KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide; gene; ss.
XX
OS *Candida albicans*.
FH Key Location/Qualifiers
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FT /codon= (seq:"ctg", aa:Ser) /codon= (seq:"ttg", aa:Tyr)
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FN US2003124134-A1.
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PD 03-JUL-2003.
XX
PP 13-SEP-2002; 2002US-00245802.
XX
PR 19-NOV-1999; 99US-0166663P.
PR 18-NOV-2000; 2000US-00715876.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX
DR WPI; 2003-810971/76.
DR P-PSDB; ABW01175.
XX
PT New monoclonal antibody against *Candida albicans* agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.
PS Disclosure; Page 46-47; 65pp; English.
XX
CC The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of *Candida*

CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX

SQ Sequence 3360 BP; 1029 A; 804 C; 520 G; 1007 T; 0 U; 0 Other;

Query Match 76.1%; Score 947.4; DB 10; Length 3360;
Best Local Similarity 85.1%; Pred. No. 2.1e-216;
Matches 1059; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

Qy	1	AAGACAATCACTGGTGTGTTTGAATGTTTAAATCAATTAACCTGTGTCACATGCTGCTAAT	60
Db	52	AAGACAATCACTGGTGTGTTTCAACAGTGTAAATCAATGCTGTGTTTAAATGCTGCTAAT	111
Qy	61	TATGCTTTCAAGGCGCAGGATACCAACTGGATGCTGTTTGGGTGGTCTTATAGT	120
Db	112	TATAATTAAGGGACACGGAACCCCACTTGGAAATGCTGTTTGGGTGGTCTTATAGT	171
Qy	121	GGTACAGTGCCTCAATCCAGGGGATACATTCATTTGAATATGCCATGTGTGTTAAATAT	180
Db	172	GGTACTAGTGCAGTCCGGGAGATACATTCATTTGAATATGCCATGTGTGTTAAATTT	231
Qy	181	ACTACTTCACAAATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAA	240
Db	232	ACTACTTCACAAATCTGTTGATTTGATGCTGCTCATGGTGTAAATATGCTACTGTCAA	291
Qy	241	TTTTATTCTGGTGAAGATTCACAACTTTTCTACATTAACATGCTGTGAACGCGCT	300
Db	292	TTTCAGGCGAGTGAAGATTTATGACCTTTTCTACATTAACATGCTGTGAGCAATACT	351
Qy	301	TTGAAATCATCATTAAGGCATTTGCTGACAGTTACTTTTACCAATGCAATTCATGTTGGT	360
Db	352	TTGACTTCATCTATTAAGGCTTTGGGTACTGCTACTTACCACTTGCATTCATGTTAGT	411
Qy	361	GGACACAGTTCATCAACTGATTTGGAAGATTCCTAAATGTTTACTGCTGGTACCAATACA	420
Db	412	GGAACTGGTTCCTCTGTTGATTTGGAAGATTCCTAAATGTTTACTGCTGGTACTAACACA	471
Qy	421	GTACATTTAATGATGGTGATTAAGATATCTCAATGATGTTGATTTGGAAGTCAACC	480
Db	472	GTACATTTAATGATGGTGGAAGAAATCTCTATTAATGTTGATTTGGAAGGTCAAAT	531
Qy	481	GTGATCCAAAGTGCAATATTTGATGCTTCCAGATTTATGCCAAGTCTCAATTAAGGTACA	540
Db	532	GTGATCCAAAGGGTACTTAATGATTTCCAGATTTATCCAAAGTCTCAACAAAGTCA	591
Qy	541	ACTCTTTTGTGGCACCAATGTGAAATGGTTACACATCTGGTACAAATGGGTTCTCC	600
Db	592	ACTCTTTTGTGGCACCAATGTGCAATGGTTACACATCTGGTACAAATGGGATTCGCT	651
Qy	601	AGTAGTACGGTGACGTTGCTATTTGATGCTCAATATTCATATTTGGTATCACAAAGGA	660
Db	652	AAACACTTATGTTGATGTTTCAAAATGACTGTTTCAAAATATTCATGTTGGTATTAACA	711
Qy	661	TTAAATGATGGAAATATCCGGTTTCATCTGAATCATTTAGTTACACTAAAATCTGTACA	720
Db	712	TTGAATGATGGAAATATCCGGTTTCATCTGAATCATTTAGTTACACCAAACTGTGTCA	771
Qy	721	TCTAATGGAATTCAGATTAATATCAAAATGACCTGCTGGTTATCGTCCATTTATGAT	780
Db	772	TCTAATGGAATTCAGATTAATATCAAAATGACCTGCTGGTTATCGTCCATTTGTTGAC	831
Qy	781	GCTTATATTTCTGCTACAGATTTAACCAATATATCTTTAGCATATACCAATGATTTACT	840
Db	832	GCTTATATTTCTGCTACAGATTTAAATTCGTACACCTGCTGATGCTAATGAATATACT	891
Qy	841	TGTCCTGGCAGTCGCTGCAAGTAACTTTCATTTAAGATGACTGGTACACAGAT	900
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Qy	1081	TATCTGACTAGACTGCGACCAATTTGGTGAACAGCTACTGTTATTTGATGTGCCATAT	1140
Db	1132	TACCTGACCAAACTTGCACCAATTTGGGAAACTGCTACTGTTATTTGATTTCCATAT	1191
Qy	1141	CATATCTACCACTGTTTACCAAGTGAATGGACAGCAACATCACTTACCAACCAACTCGT	1200
Db	1192	CACACTACCACTGTTTACCAAGTGAATGGACAGCAACATCACTTCCACCAACACAT	1251
Qy	1201	ACCAATCCAACTGATTCATTTGACACAGTGGTGTGACTAGTTCCA	1245
Db	1252	ACTAATCCAACTGATTCATTTGACACAGTGGTGTGACTAGTTCCA	1296

RESULT 5

AAD62306
ID AAD62306 standard; DNA; 1404 BP.

XX AAD62306;

XX 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 2 gene.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide; gene; ss.

XX Candida albicans.

XX Key Location/Qualifiers

FT CDS 1..1404

FT /tag= a

FT /product= "C. albicans ALS protein"

FT /transl_except= {pos:121..123, aa:Lys}

FT /codon= (seq:"ctg", aa:Ser)

FT /note= "No stop codon"

FT /partial

XX US2003124134-A1.

XX 03-JUL-2003.

XX 13-SEP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

XX 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX P-PSDB; ABW01169.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.

XX Disclosure; Page 17-18; 65pp; English.

XX The present invention relates to a monoclonal antibody against an

CC agglutinin-like sequence (ALS)1 protein that specifically binds an

CC epitope in an N-terminal domain and which inhibits adherence of Candida

CC albicans to endothelial cells. The invention is useful as vaccines for

CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX
SQ Sequence 1404 BP; 422 A; 269 C; 252 G; 461 T; 0 U; 0 Other;

Query Match 71.9%; Score 895; DB 10; Length 1404;
Best Local Similarity 83.2%; Pred. No. 5.7e-204;
Matches 1031; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

QY 7 ATCACTGGTGTGTTTGTAGTATTTAAATTCATTAACTGGTCCAAATGCTGCTAAATATGCT 66
DB 58 ATACGGGTGTTTCAATAGTATTTGATTCGTTGACATGGACAAGAGCTGGAATATATGCT 117
QY 67 TTCAAAGGCCAGATACCCAACTTGAATGCTGTTTGGGTGGTCTTAGAGTGATCC 126
DB 118 TATAACGGCCCAATATAGACCAACTTGAATGCTGTTTGGGCTGGTCTTTAGATGGTACT 177
QY 127 AGTCCCAATCCAGGGGATACATTCCACATTCGAATGCAATGCTGTTGTTAAATATATCTACT 186
DB 178 AGTGCAATCCAGAGACACATTCACATTCGAATGCAATGCTGTTTAAATATTTATACC 237
QY 187 TCACAAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAATTTTAT 246
DB 238 GATCAACATCTGTTGATTTGACTGCTGAAGGTGTTAAATATGCTACATGCTCAGTTTAT 297
QY 247 TCTGGTGAAGATTCACAACTTTTCTACATTAACATGACTGTGAACGAGCTTTGAAA 306
DB 298 TCAGGTGAAGAAATTTACAACTTTTCTCAATTAATGTAATGAGCAATATCTTTAACA 357
QY 307 TCATCCATTAAGGATTTGGTACAGTTTACTTTTACCAATTCGATTCATTAATGTTGGTGAACA 366
DB 358 TCATCTATTAAAGCTTTGGGTACGGTTACTTTTACCAATTTCAATTAATGTTGGTGAACA 417
QY 367 GGTTCATCACTGATTTGGAGATTTTAAATGTTTACTGCTGTACCAATACAGTACACA 426
DB 418 GGTTCATCGTGTGATTTGGAAAGTTCTCAATGTTTAAAGGCTGGCACCACACAGTTTACT 477
QY 427 TTTAATGATGATTAAGATATCTCAATGATGTTGAGTTGAAAGTCAACGTTGAT 486
DB 478 TTTAATGATGATTAAGATATCTCAATGATGTTGAGTTGAAAGTCAACGTTGAT 537
QY 487 CCAAGTGCATATTTGATGCTTCAGAGTTATGCAAGTTCATTAAGGTTCAACACTCTT 546
DB 538 CCAAGTGCATATTTGATGCTTCAGAGTTATGCAAGTTCATTAAGGTTCAACACTCTT 597
QY 547 TTTGTGGCACCACCAATGTGAAATGGTTTACATCTGTGTAACATGGGGTTCTCCAGTAGT 606
DB 598 TATGTGGCACCACCAATGTGAAATGGTTTACATCTGTGTAACATGGGGTTCTCCAGTAGT 657
QY 607 AACGGTGAAGTGTATGATGCTCAAAATTTTCAATTTGATGATCAAAAGGATTAAT 666
DB 658 ACTGGTGACACTACTATTGACTGTTTCAAAATGTTTCAATTTGATGATCAAAAGGATTAAT 717
QY 667 GATTGGAAATTCGGTTTCAATCTGAATTCATTTAGTTACACTAAACTTGTACATCTAAT 726
DB 718 GATTGGAAATTCGGTTTCAATCTGAATTCATTTAGTTACACTAAACTTGTACATCTAAT 777
QY 727 GGAATTCAGATTAATATCAAAATGTATCTGCTGTTATGCTCCATTTATGATGCTTAT 786
DB 778 GGTATTTCTATACATATGAATAATGTCCCGCTGGTTATCGTCCATTTTGTGAGGTATAT 837
QY 787 ATTTCTGTACAGATGTTTAAACCAATATCTTTAGCATATACCAATGATGATGCTGCT 846
DB 838 ACTCTGGTGTGAGGCCAAGACAGACA---ATTAAGATATATCTAATGATTATGCTGTTGT 894
QY 847 GCGAGTCTGCTGCAAAATGAACCTTTTCACTTTTAAGATGGAATGGAATCAAGAAATAGTAT 906
DB 895 GGTAGTCTCTTCAAAAGTAAAGCGTTTCAATTTAAGATGAGGATACAAATATAGTAA 954
QY 907 GCCCGATCAACGGTATTTGCTCAATTTGCTGCTCAACAGTACAGACAGTACCACT 966

DB 955 GCTAATCTTAACGGTTTTGTCTCATTTGTTGTCTACAACCCGAAACAGTTTACTGACAGTACTACT 1014
QY 967 GCTGTCACTACTTTTACCAATTCATTCACAGTGTGTGATAAACCAAAACAATTCGAAATTTTG 1026
DB 1015 GCTGTCACTACTTTTACCTTTTATCCAGTGTGTGACAAACCAAAACAATTCGAAATTTTG 1074
QY 1027 CAACCTATTCCAAACCACTACCATCAACATTCATATGTTGGTGTGACTACTTCTCTATCTG 1086
DB 1075 CAACCTATTCCAAACCACTACCATCAACATTCATATGTTGGTGTGACTACTTCTCTATCTG 1134
QY 1087 ACTAAGACTGCAACCAATTCGTTGAAACAGTACTGTTATTTGTTGATGTCATATCATACT 1146
DB 1135 ACTAAGACTGCAACCAATTCGTTGAAACAGTACTGTTATTTGTTGATGTCATATCATACT 1194
QY 1147 ACCCAACTGTTTACCAGTGAATGGACAGGAACAATCACTTACCACCAACAATTCGTACCAAT 1206
DB 1195 ACCCAACTGTTTACCAGTGAATGGACAGGAACAATCACTTACCACCAACAATTCGTACCAAT 1254
QY 1207 CCAACTGATTCATTTGACACAGTGGTGGTACAAAGTTCCA 1245
DB 1255 CCAACTGATTCATTTGACACAGTGGTGGTACAAAGTTCCA 1293

RESULT 6

AAD62308

ID AAD62308 standard; DNA; 1407 BP.

XX AAD62308;

XX 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 4 gene.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX candidiasis; vaccine; fungicide; gene; ss.

XX Candida albicans.

XX Key Location/Qualifiers

XX CDS 1. .1407

XX /tag= a

XX /product= "C. albicans ALS protein"

XX /codon= (seq:"ctg", aa:Ser)

XX /note= "No stop codon"

XX /partial

XX US2003124134-A1.

XX 03-JUL-2003.

XX 13-SEP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

XX 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX P-PSDB; ABW01171.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
XX 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
XX candidiasis, or to generate an immune response that blocks adherence of
XX the organism.

XX Disclosure; Page 24; 65pp; English.

XX The present invention relates to a monoclonal antibody against an

XX agglutinin-like sequence (ALS)1 protein that specifically binds an

XX epitope in an N-terminal domain and which inhibits adherence of Candida

XX albicans to endothelial cells. The invention is useful as vaccines for

CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX

SQ Sequence 1407 BP; 391 A; 294 C; 253 G; 469 T; 0 U; 0 Other;

Query Match 58.9%; Score 733.4; DB 10; Length 1407;
Best Local Similarity 74.5%; Pred. No. 2.6e-165;
Matches 923; Conservative 0; Mismatches 316; Indels 0; Gaps 0;

QY 7 ATCACTGCTGTTTGTAGTATTAATTCATTAATCTGGTCCAAATGCTGCTAATATGCT 66
DB ATTAACAGGTGTTTCAATAGTATTAATTCGTTAACTTGGGCCAAATGCTGCTTCTTATCCA 117
QY 67 TTCGAAGGCCAGGATACCCCACTGGATGCTGTTTGGGTGCTCTAGAGTGAACC 126
DB 118 TATAGAGGTCCAGCTACTCTCTACTTGGACCCCTGTAATAGGATGGCTCTTTAGATGGAGCT 177
QY 127 AGTGCATCCAGGGGATACATTCACATTTGAATATGCCATCTGTGTTTAAATATATACTACT 186
DB 178 ACTGCTAGTGTGTGACACATTCAGGTTAGACATGCTTGTGTTTCAAAATTTATTA 237
QY 187 TCACAAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAATTTAT 246
DB 238 GATCAAAAGCTCAATGATTTAGTTGCTGATGCTGCTACTTATGCTACTTGTAAATTTGAAT 297
QY 247 TCTGTGTAAGAAATTCACAACTTTTCTACATTAACATGCTACTGTGAACGAGCTTTGAA 306
DB 298 TCTGCCGAAGAGTTTACTACTTTTCTAGTGTGTCATGCTACTGTGACTACTACATGACT 357
QY 307 TCATCCATTAAGGCATTTGGTACAGTTACTTTTACCAATTCATCAATGTTGGTGAACA 366
DB 358 GCTGACACAAAGCCATAGGAACCTGTAACATTAACCTTTCTCATTCAGTGTGGGGATCA 417
QY 367 GGTTCATCACTGATTTTGGGAAGATTTCTAAATGTTTACTGCTGTGTAACCAATACAGTCA 426
DB 418 GGTTCAGATGTTGATTTGGCAATTTCTCAATGTTTACTGCGAGGAATCAATACAGTTACT 477
QY 427 TTTAATGATGTTGATTAAGATATCTCAATGATGTTGATGTTGAAAGTCAACCGTTGAT 486
DB 478 TTTAATGATGTTGATTAAGATATCTCAATGATGTTGATGTTGAAAGTCAACCGTTGAT 537
QY 487 CCAAGTGCATATTTGATGCTTCCAGATTTAGCAAGTTCAGCAATCAATGATGCTCAACTCT 546
DB 538 TCCAGCGATCGTATCTGTTGTCAGGAATTTTACCAGTCTTTTCAAGCAGTAAATCTT 597
QY 547 TTTGTGGCACCAATGTTGMAAATGTTTACACATCTGTTACAAATGGGTTCTTCCAGTATG 606
DB 598 TTTCTTCCCAAGATGTTGCAATGTTTATCTTCTGTTACAAATGGGATTTTCCAGTCT 657
QY 607 AACGTTGAGTGTGCTATGATGCTCAATATATTCATATGTTGTTATCAAAAGGATTAAT 666
DB 658 GGTACTGTTGCTACTATAGATTTGTTCCAGTTCATGTCGGGATATCAATGGGTTGAAT 717
QY 667 GATTCGAATATCCGGTTTTCATCGAATCAATTTAGTACACTTAAATCTGTACATCTAAT 726
DB 718 GATTCGAATATCCAAATTTTCACTGGAATCTTTTCTTACCAAGACCTGTATACATCA 777
QY 727 GGAATTCAGATTAATATATCAAAATGTTTACCTGCTGTTATCGTCCATTTTATGATCTTAT 786
DB 778 AGTGTTTTATGTTAATCTTTTCAAAATGTTCTGCGGATATCGTCCATTTTGTGATGCTTAT 837
QY 787 ATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATATATCTTGTCT 846
DB 838 ATTTCTGCAACAGGATGCTCATATACCATGCAATACACTTAATATATATATGTTGTT 897
QY 847 GGCAGTCTGCTGCAAGTAAACCTTTTCACTTTAAGATGCACTGGATACAGATATGATAT 906
DB 898 GCGCGGCTTCTGTTGATGACTCAATTTACTACTTGGCGGGGATATAGTAATAGTCA 957
QY 907 GCGGATCTAACCGTATTTGCTATTTGTTGCTCAACTAGACAGTTTACAGAGTACCACT 966

DB 958 GCTGGTTCATTAATGGTATTATACCAATTTGGTAACTAGAACAGTTACAGACAGTACCAC 1017
QY 967 GCTGTCACTACTTTTACCAATTCATTCAGAGTGTGTTGATATAAAACCAAAACAAATCGAAATTT 1026
DB 1018 GCTGTGACTACTTTTACCAATTCATTCGATACGACAAACCAAAACAAATCGAAATTTT 1077
QY 1027 CAACCTATTTCACCACTACTACATCAAACTTATGTTGGTGTGACTACTTCTATCTG 1086
DB 1078 CAACCTATTTCACCACTACTACATTCATTAATGTTGGTGTGACAACTTCTTACCTG 1137
QY 1087 ACTAAGACTCCCAATTTGGTGAACAGCTACTGTTATTTGATGTGCCATATCATACT 1146
DB 1138 ACTAAAACCTGCACCAATTTGGTGAACAGCTACTGTTATTTGATGTGCCATATCATACT 1197
QY 1147 ACCAACAATCTTTACCACTGATGACAGGAACTCACTACCACTCACTGTTGTTGTTGTT 1206
DB 1198 ACTAACAATCTTTACCACTGATGACAGGAACTCACTACCACTCACTGTTGTTGTTGTT 1257
QY 1207 CCAACTGATTCATTAATGACAGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1245
DB 1258 CCAACTGATTCATTAATGACAGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1296

RESULT 7

AAD62313
ID AAD62313 standard; DNA; 1404 BP.

XX AAD62313;

XX 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 9 gene.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX candidiasis; vaccine; fungicide; gene; ss.

XX Candida albicans.

XX Key Location/Qualifiers

XX CDS 1..1404

XX /*tag= a

XX /product= "C. albicans ALS protein"

XX /codon= (seq:"ctg", aa:Ser) /codon= (seq:"ttg", aa:Tyr)

XX /note= "No stop codon"

XX /partial

XX US2003124134-A1.

XX 03-JUL-2003.

XX 13-SEP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

XX 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX P-PSDB; ABW01176.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence

XX 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated

XX candidiasis, or to generate an immune response that blocks adherence of

XX the organism.

XX Disclosure; Page 50-51; 65pp; English.

XX The present invention relates to a monoclonal antibody against an

XX agglutinin-like sequence (ALS)1 protein that specifically binds an

XX epitope in an N-terminal domain and which inhibits adherence of Candida

XX albicans to endothelial cells. The invention is useful as vaccines for

CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) gene
XX
SQ

Sequence 1404 BP; 413 A; 286 C; 253 G; 452 T; 0 U; 0 Other;

Query Match 57.3%; Score 713.8; DB 10; Length 1404;
Best Local Similarity 73.9%; Pred. No. 1.3e-160;
Matches 920; Conservative 0; Mismatches 322; Indels 3; Gaps 1;
Qy 1 AAGCAATCACTGCTGTTTGTAGTATTTAAATTCATTAATCTGGTCCCAATGCTGCTAAT 60
Db 52 AAAAATATTAATGCTGTTTCAATAGTATTTGACTCATTCATGACATGACATAGATCCGTTGAA 111
Qy 61 TATGCTTTCAAGGGCCAGGATACCCCAATGGAATGCTGTTTGGGTTGCTGCTTAGAT 120
Db 112 TATGCTTTCAAGGGCCAGGATACCCCAATGGAATGCTGTTTGGGTTGCTGCTTAGAT 171
Qy 121 GGTACCAAGTCCCAATCCAGGGGATACATTCACATTTGAATATGCCATGCTGTTTAAATAT 180
Db 172 AGTACCACTGCTGACCCAGGAGACACATTCACCTTGATTTTGCTTGCTGATTTAAATTT 231
Qy 181 ACTACTTCACAAATCATCTGTTGATTAATTCGCCGATGGTGTAAATATGCTACTTGTCAA 240
Db 232 ATAACTACCCAAACATCTGTTGATTTGACTGCTGATGGTGTAGCTATGCCCACCTTGTGAC 291
Qy 241 TTTTATTTCTGTTGAAGAAATTCACAACTTTTCTACATTTAAATGATGCTGTAAGACGCT 300
Db 292 TTTTAAATGCTGTTGAAGAAATTTACGACATTTTCTTCTTATCATGATGCTGTAAGACGCT 351
Qy 301 TTGAAATCATCCATTAAGGCAATTTGGTACAGTACTTTTACCAATTCATTCATTTGGT 360
Db 352 TCGTATCATATGCTAGGTTTCTGTTACGTTCAATTTGCCATTAATTCATTCATTTAGT 411
Qy 361 GGAACAGGTTCAATCAATGATTTGGAAGATTTCAATATGTTTACTGCTGTTACCAATACA 420
Db 412 GGAACAGGTTCTTCAGTTGATTTGGCAGATTCCAATGTTTACTGCGGAAAAACACT 471
Qy 421 GTCAATTTAATGATGCTGATAAGATATCTCAATGATGTTGATTTGAAAGTCAACC 480
Db 472 GTGACTTTTCATGATGCGGATACAAAGATTTCTACCACTGTTGATTTGACGGTCTCCA 531
Qy 481 GTTCATCCAAAGTGCATATTTGTATGCTTCCAGAGTTATGCCAGTCTCAATATAAGGTCA 540
Db 532 GTATACCCAGTGTATATATACAGCTCAGAAATATTCCTAGTCTCAATATAAATTTCA 591
Qy 541 ACTCTTTTGGGCCACCAATGTAAGTGAATGTTTACACATCTGTTCAATGCGGTTCTCC 600
Db 592 AGTCTTTTGGTGGCCCAATGTAAGATGTTTACACATCTGTTAATGCGGATTTGTA 651
Qy 601 AGTATGACGTTGCTGCTGTTGATTTGATTTGCTCAATATTCATATGTTGTTACCAAGGA 660
Db 652 GCTAGTAACGGT---GCTCATTTGATTTGCTCAATGTTCAATATAGGAATATCAAAAGGT 708
Qy 661 TTAATGATTTGGAATTTCCGGTTTTCATCTGAATCATTTAGTTTACACTAAACTTTTACA 720
Db 709 TTAATGATTTGGAATTTCCAGTAAGTTTCAGAAATCATTTCTTACACGAAATCTTTGAC 768
Qy 721 TCTAATGGAATTCAGATTAATATCAAAATGTAACCTGCTGTTATGCTTATGCTTATTTAT 780
Db 769 TCAACCAAGTATTAACAGTTGAAATTTCAAAATGTTTCTGCTGGTATCGCCCTTTTGTGAT 828
Qy 781 GCTTATATTTCTGCTACAGATTTTAAACCAATATATTTAGCATATACCAATGATTTACT 840
Db 829 GCATATATTTCTGAGAAATATTTGATAAATATATACCTTGAGTACGCAATATGATATACT 888
Qy 841 TGTCGTGCGAGTCTGTCGAAATGTAACCTTTTCACTTTAAGATGGAATGGAATACAGAAAT 900
Db 889 TGTGAAATGCAATATCTGTTGTTGATCCATTTACTTTTAAATGTTGGGGGTATATAAAC 948
Qy 901 AGTCAATGCCGATTTAAAGGTTATTTGCTATGTTGCTCAACTGAAACAGTTACAGACGT 960

Db 949 TCTGAAGCAGACTCTGACGGGATGTGATCGTAGTTTACAAACAGAACTGTCACAGACAGT 1008
Qy 961 ACCACTGCTGTCACTACTTTTACATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1020
Db 1009 ACAACAGCTGTGACTACTTTTACCTTTCAATCCAAAGTGTGATAAAACCGAAACAAATTGAA 1068
Qy 1021 ATTTTGAACCTTATTCACCACTACCATCACAATTCATATATGTTGTTGTTGTTGTTGTTGTT 1080
Db 1069 ATTTTGAACCTTATTCACCACTACCATCACAATTCATATATGTTGTTGTTGTTGTTGTTGTT 1128
Qy 1081 TATCTCACTAAGACTGCACCAATTTGGTGAAGCAAGCTACTGTTATTTGTTGTTGTTGTTGTTGTT 1140
Db 1129 TATGAACATTAACCGGAACAATTTGGTGTACTGCGAGAGTCAATTCGATACACCTTAT 1188
Qy 1141 CATACTACCACTGTTTACCAGTGAATGGACAGGAACAATCACTACCACTACCACTCGT 1200
Db 1189 CATATCACTGCCACTGTTACAAATTTCTGAGTGGGTCAATTACAACTACCACTACTTAT 1248
Qy 1201 ACCAATCCAACTGATTCATTTGACACAGTGGTGGTACAAAGTTCCA 1245
Db 1249 ACTAATCCCACTGGTTCCATAGACACTGTTATTTGTCGAAATTTCCA 1293

RESULT 8

AAD62310
ID AAD62310 standard; DNA; 4332 BP.

XX AAD62310;

XX AC AC (first entry)

DT 15-JAN-2004

XX Candida albicans agglutinin-like sequence (ALS) 6 gene.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX candidiasis; vaccine; fungicide; gene; ss.

XX Candida albicans.

XX Key

XX CDS

XX 1. .4332

XX /tag= a

XX /product= "C. albicans ALS protein"

XX /transl_except= (pos:1..3, aa:Met)

XX /codon= (seq:"ctg", aa:Ser) /codon= (seq:"ttg", aa:Tyr)

XX US2003124134-A1.

XX 03-JUL-2003.

XX 13-SEP-2002; 2002US-00245802.

XX 19-NOV-1999; 99US-0166663P.

XX 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX P-PSDB; ABW011173.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
XX 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
XX candidiasis, or to generate an immune response that blocks adherence of
XX the organism.
XX Disclosure; Page 31-33; 65pp; English.

XX The present invention relates to a monoclonal antibody against an

XX agglutinin-like sequence (ALS)1 protein that specifically binds an
XX epitope in an N-terminal domain and which inhibits adherence of Candida
XX albicans to endothelial cells. The invention is useful as vaccines for
XX treating and preventing disseminated candidiasis and for generating an

[illegible]

```
OY 1119 TGTATTGTTGATGCGCATATCATCTACTACACCAACTGTTACCACTGTAATGACAGGAAC 1178
DB 100 TGTATTGTTGATGTTCCATATCACACTACCACTGTTACTAGTGAATGACAGGAAC 41

OY 1179 AATCACTACCAACCACTGTTACCAATCCAACTGATTCA 1218
DB 40 AATCACTACTACTACACACAACTAATCCACAGGTTCA 1

RESULT 11
AAQ62590/c
ID AAQ62590 standard; DNA; 100 BP.
XX
AC AAQ62590;
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1994 (first entry)
XX
XX Candida albicans-specific hybridisation probe.
XX
XX DNA hybridisation probe; detection; assay; C.albicans yeast;
XX species specific sequence; ss.
XX
XX Candida albicans.
OS
XX EP595167-Al.
PN
XX
XX 04-MAY-1994.
PD
XX
XX 19-OCT-1993; 93EP-00116865.
PF
XX
XX 30-OCT-1992; 92DE-04236708.
PR
XX
XX (FARB ) BAYER AG.
PA
XX
XX Springer W, Plempel M, Loebberding A;
PI
XX
XX WPI; 1994-145805/18.
DR
XX
XX New hybridisation reagents specific for Candida albicans - are
PT polynucleotide and oligo:nucleotide probes, providing high sensitivity
PT and early diagnosis of infection.
PT
XX
XX Claim 9; Page 33; 44pp; German.
PS
XX
XX A C.albicans gene library was prepared in pBR322 and inserts were
CC selected for multiple presence in the genome, strong conservation without
CC deletions or insertions and absolute specificity for C.albicans. Gene
CC probe 431.19 (AAQ62552) hybridised to all but 4 of the 87 clinical
CC isolates of C.albicans being tested. A clone (436.1) was then isolated
CC from the 4 isolates not recognised by 431.19. Some 100mer
CC oligonucleotides covering the complete sequences of 431.19 and 436.1 were
CC synthesised and tested (see AAQ62558-Q62594). All were found to be
CC absolutely specific for C.albicans. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX SQ Sequence 100 BP; 31 A; 17 C; 19 G; 33 T; 0 U; 0 Other;
XX
XX Query Match 6.6%; Score 82.4; DB 2; Length 100;
XX Best Local Similarity 89.0%; Pred. No. 6.5e-10;
XX Matches 89; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 919 GGTATTGTCATTTGTTGCTACAACTAGACAGTTACAGACAGTACCTGCTGTGACTACT 978
DB 100 GGTATTGTCATTTGCTGCTACAACTAGACAGTTACAGATAGTACTGCTGTGACTACT 41

OY 979 TTACCATTCATCCCAAGTGTTCATATAAACCACCAATCG 1018
DB 40 TTACCATTCATTCGATGTTGACAAAACATAAAACAATTG 1

RESULT 12
AAQ62589/c
ID AAQ62589 standard; DNA; 100 BP.
XX
AC AAQ62589;
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1994 (first entry)
XX
XX Candida albicans-specific hybridisation probe.
XX
XX DNA hybridisation probe; detection; assay; C.albicans yeast;
XX species specific sequence; ss.
XX
XX Candida albicans.
OS
XX EP595167-Al.
PN
XX
XX 04-MAY-1994.
PD
XX
XX 19-OCT-1993; 93EP-00116865.
PF
XX
XX 30-OCT-1992; 92DE-04236708.
PR
XX
XX (FARB ) BAYER AG.
PA
XX
XX Springer W, Plempel M, Loebberding A;
PI
XX
XX WPI; 1994-145805/18.
DR
XX
XX New hybridisation reagents specific for Candida albicans - are
PT polynucleotide and oligo:nucleotide probes, providing high sensitivity
PT and early diagnosis of infection.
PT
XX
XX Claim 9; Page 33; 44pp; German.
PS
XX
XX A C.albicans gene library was prepared in pBR322 and inserts were
CC selected for multiple presence in the genome, strong conservation without
CC deletions or insertions and absolute specificity for C.albicans. Gene
CC probe 431.19 (AAQ62552) hybridised to all but 4 of the 87 clinical
CC isolates of C.albicans being tested. A clone (436.1) was then isolated
CC from the 4 isolates not recognised by 431.19. Some 100mer
CC oligonucleotides covering the complete sequences of 431.19 and 436.1 were
CC synthesised and tested (see AAQ62558-Q62594). All were found to be
CC absolutely specific for C.albicans. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX SQ Sequence 100 BP; 31 A; 17 C; 19 G; 33 T; 0 U; 0 Other;
XX
XX Query Match 6.6%; Score 82.4; DB 2; Length 100;
XX Best Local Similarity 89.0%; Pred. No. 6.5e-10;
XX Matches 89; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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ID AAQ62589 standard; DNA; 100 BP.
XX
AC AAQ62589;
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1994 (first entry)
XX
XX Candida albicans-specific hybridisation probe.
XX
XX DNA hybridisation probe; detection; assay; C.albicans yeast;
XX species specific sequence; ss.
XX
XX Candida albicans.
OS
XX EP595167-Al.
PN
XX
XX 04-MAY-1994.
PD
XX
XX 19-OCT-1993; 93EP-00116865.
PF
XX
XX 30-OCT-1992; 92DE-04236708.
PR
XX
XX (FARB ) BAYER AG.
PA
XX
XX Springer W, Plempel M, Loebberding A;
PI
XX
XX WPI; 1994-145805/18.
DR
XX
XX New hybridisation reagents specific for Candida albicans - are
PT polynucleotide and oligo:nucleotide probes, providing high sensitivity
PT and early diagnosis of infection.
PT
XX
XX Claim 9; Page 33; 44pp; German.
PS
XX
XX A C.albicans gene library was prepared in pBR322 and inserts were
CC selected for multiple presence in the genome, strong conservation without
CC deletions or insertions and absolute specificity for C.albicans. Gene
CC probe 431.19 (AAQ62552) hybridised to all but 4 of the 87 clinical
CC isolates of C.albicans being tested. A clone (436.1) was then isolated
CC from the 4 isolates not recognised by 431.19. Some 100mer
CC oligonucleotides covering the complete sequences of 431.19 and 436.1 were
CC synthesised and tested (see AAQ62558-Q62594). All were found to be
CC absolutely specific for C.albicans. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX SQ Sequence 100 BP; 24 A; 11 C; 29 G; 36 T; 0 U; 0 Other;
XX
XX Query Match 6.1%; Score 76; DB 2; Length 100;
XX Best Local Similarity 85.0%; Pred. No. 2.2e-08;
XX Matches 85; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 1019 AAATTTTGCACCTATTTCACCACTACCACTTCCATCATATGTTGGTGTGACTACTT 1078
DB 100 AAATTTTGCACCCCATTCACCAACTACCACTACCACTATATGTTGGTGTGACTACTT 41

OY 1079 CCTATCTGACTAAGACTGCACCAATTTGTTGTAACAGCTAC 1118
DB 40 CCTACAGAACCCAAACTGTACCAATAGACAACTGCTAC 1

RESULT 13
AAQ62592/c
ID AAQ62592 standard; DNA; 100 BP.
XX
AC AAQ62592;
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1994 (first entry)
XX
XX Candida albicans-specific hybridisation probe.
XX
XX DNA hybridisation probe; detection; assay; C.albicans yeast;
XX species specific sequence; ss.
```



```
XX OS Candida albicans.
XX PN EP595167-A1.
XX PD 04-MAY-1994.
XX XX
XX PF 19-OCT-1993; 93EP-00116865.
XX PR 30-OCT-1992; 92DE-04236708.
XX PA (FARB ) BAYER AG.
XX PI Springer W, Plempel M, Loebberding A;
XX DR WPI; 1994-145805/18.
XX XX
XX FT New hybridisation reagents specific for Candida albicans - are
XX PT polynucleotide and oligo:nucleotide probes, providing high sensitivity
XX FT and early diagnosis of infection.
XX PS Claim 9; Page 34; 44pp; German.
XX CC A C.albicans gene library was prepared in pBR322 and inserts were
XX CC selected for multiple presence in the genome, strong conservation without
XX CC deletions or insertions and absolute specificity for C.albicans. Gene
XX CC probe 431.19 (AAQ62552) hybridised to all but 4 of the 87 clinical
XX CC isolates of C.albicans being tested. A clone (436.1) was then isolated
XX CC from the 4 isolates not recognised by 431.19. Some 100mer
XX CC oligonucleotides covering the complete sequences of 431.19 and 436.1 were
XX CC synthesised and tested (see AAQ62558-Q62594). All were found to be
XX CC absolutely specific for C.albicans. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 100 BP; 39 A; 15 C; 19 G; 27 T; 0 U; 0 Other;
Query Match 5.5%; Score 68; DB 2; Length 100;
Best Local Similarity 80.0%; Pred. No. 1.8e-06;
Matches 80; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 719 CATCTAATGGAATTCAGATTAATATCAAAATGTAACCTGCTGGTATCGTCATTATTCG 778
DB 100 CATCTAATGGAATTCATCATATGAAATATCCCTGCGAGGTATCGTCATTATTCG 41
QY 779 ATGCTTATATTTCTGCTACAGATGTTAAACCAATATCTTT 818
DB 40 ACGTTTATGATCTGCTCCGATGTTAAACGATATATTTT 1
RESULT 14
AAA61847
ID AAA61847 standard; DNA; 5511 BP.
XX AC AAA61847;
XX DT 28-OCT-2000 (first entry)
XX DE Cryptosporidium parvum Iowa isolate GP900 ORF.
XX KW GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis;
XX KW competitive inhibition; attachment; invasion; ligand binding; sporozoite;
XX KW merozoite; diarrhoea; protozoa; open reading frame; ORF; ds.
XX OS Cryptosporidium parvum.
XX FH Key Location/Qualifiers
XX FT 1..5511
XX FT CDS /*tag= a
XX FT /product= "Cryptosporidium parvum Iowa isolate GP900"
XX FT /note= "No stop codon given"
XX PN US6071518-A.
XX XX
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PD 06-JUN-2000.
XX 12-SEP-1997; 97US-00928361.
XX 29-MAY-1992; 92US-00891301.
XX PR 01-JUN-1993; 93US-00071880.
XX PR 03-APR-1995; 95US-00415751.
XX PR 14-AUG-1996; 96US-00700651.
XX PR 13-SEP-1996; 96US-0026062P.
XX (REGC ) UNIV CALIFORNIA.
XX Petersen C;
XX WPI; 2000-422065/36.
XX DR P-PSDB; AAB11726.
XX XX
XX FT New GP900 protein fragments and fusion proteins of Cryptosporidium
XX PT parvum, useful for detecting the presence of the parasite, and diagnosing
XX FT or treating Cryptosporidium infections by competitive inhibition of the
XX FT function of GP900.
XX PS Claim 16; Col 37-42; 59pp; English.
XX CC The invention relates to the GP900 glycoprotein of the protozoan
XX CC Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion
XX CC proteins comprising GP900 fragments. The invention also relates to the
XX CC administration of GP900 or fragments thereof to a host to elicit anti-
XX CC GP900 antibody production, and to a method of cryptosporidiosis treatment
XX CC or prophylaxis comprising administration of anti-GP900 antibodies to an
XX CC individual. Cryptosporidium parvum GP900 and GP900 fragments are able to
XX CC competitively inhibit sporozoite or merozoite attachment or invasion, and
XX CC are also useful for the generation of anti-GP900 antibodies. The
XX CC antibodies also inhibit sporozoite or merozoite attachment/invasion and
XX CC additionally inhibit the binding of GP900 ligands to GP900. GP900
XX CC proteins, fragments and antibodies may therefore be used to treat or
XX CC prevent cryptosporidiosis. Infection with Cryptosporidium is a common
XX CC cause of diarrhoea in humans and causes life-threatening diarrhoea in
XX CC immunocompromised persons. Cryptosporidiosis can be contracted from
XX CC contaminated municipal water supplies (e.g., public swimming pools). It
XX CC is also a cause of disease in animals, resulting in financial losses in
XX CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
XX CC used for the diagnosis of Cryptosporidium parvum infections, and for the
XX CC detection of the parasite in the environment. The present sequence
XX CC represents the open erasing frame (ORF) encoding the GP900 protein of the
XX CC Iowa isolate of Cryptosporidium parvum
XX SQ Sequence 5511 BP; 1964 A; 1204 C; 944 G; 1399 T; 0 U; 0 Other;
Query Match 4.9%; Score 61.4; DB 3; Length 5511;
Best Local Similarity 50.9%; Pred. No. 0.00021;
Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
QY 933 TGCTACAACGTAGAACAGTTACAGACAGTACCACTGCTGTCCTACTTTTACCACTTCATCC 992
DB 1035 TACTACTACGACAAACCAACCACTACTACTACTACTACTACTACTACTACTACTACTAC 1094
QY 993 AAGTGTGTGATATAAAACCAAAACCAATCGAAATTTTGCACACCTATTTCACCACTACCATCAC 1052
DB 1095 CAGCACTACTACCAACCAACCACTACCAAGAACCAACCAACCAACCAACCAACCAAC 1154
QY 1053 AACTTCATATGTTGGTGTGACTACTTCTTCTATCTGATAGACTGACCAATGGTGAAC 1112
DB 1155 AACTTACTACTACTACCAACCAACCACTACTACTACTACTACTACTACTACTACTACTAC 1214
QY 1113 AGTACTGTTATTTGTTGATGTCGCATATCATACTACCAACCTGTTACCACTGAATGAC 1172
DB 1215 TACTACTACTACTACTACTACCAACCAACCACTACTACTACTACTACTACTACTACTACT 1274
QY 1173 AGGAACAATCACTTACCACCACTGCTGATCACTCAATCCAACTGATTCAA 1219
DB 1275 AACCAACCAACCAACCAACCACTACTACTACTACTACTACTACTACTACTACTACTACT 1321
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Search completed: March 23, 2005, 10:45:49
Job time : 526 secs

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RESULT 15
ABT04776
ID ABT04776 standard; DNA; 5511 BP.
XX AC
XX ABT04776;
XX DT
XX 27-SEP-2002 (first entry)
XX DE
XX C parvum GP900 gene fragment SEQ ID NO: 2.
XX KW
XX Cryptosporidium detection; GP900; P68; cryptopain; cryptosporidiosis;
XX gene; ds.
XX OS
XX Cryptosporidium parvum.
XX FN
XX WO200194631-A1.
XX PD
XX 13-DEC-2001.
XX PF
XX 14-MAY-2001; 2001WO-US015624.
XX PR
XX 06-JUN-2000; 2000US-00588995.
XX PA
XX (REGC ) UNIV CALIFORNIA.
XX PI
XX Petersen C, Barnes DA, Nelson RG, Gut J;
XX DR
XX WPI; 2002-566447/60.
XX CC
XX Detecting Cryptosporidium in biological and environmental samples and
XX diagnosis of cryptosporidiosis involves, contacting the sample with
XX Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA.
XX PS
XX Disclosure; Page 99-101; 157pp; English.
XX CC
XX The present invention relates to a method of detecting Cryptosporidium in
XX biological and environmental samples, and of diagnosing
XX cryptosporidiosis. This involves obtaining a sample and contacting it
XX with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or
XX RNA, or its variant, mutant or fragment. The method is also useful for
XX detecting and identifying individual Cryptosporidium isolates based on
XX the genetic characteristics, and for diagnosis of prior or concurrent
XX Cryptosporidium infection. The present sequence is a C. parvum coding
XX sequence used in the exemplification of the invention
XX SQ
XX Sequence 5511 BP; 1964 A; 1204 C; 944 G; 1399 T; 0 U; 0 Other;
XX
XX Query Match 4.9%; Score 61.4; DB 6; Length 5511;
XX Best Local Similarity 50.9%; Pred. No. 0.00021;
XX Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
QY 933 TGCTAACTAGAACAGTTACAGACAGTACCACTGCTGCTACTACTTTTACCATTCAATCC 992
DB 1035 TACTACTAGCACACCAACCAACTACTACTACTACTACTACTACTACTACTACTACT 1094
QY 993 AAGTGTGATAAACCAAAACATCGAAATTTTGGCACTATTCCAACTACCACTAC 1052
DB 1095 CACGACAACTACCAACCAACCACTACCAAGAAACCAACCAACCAACCAACCAAC 1154
QY 1053 AACTTCATATGTTGGTGTGACTACTTCTATCTGACTAAGACTGCACCAATTTGGTGAAC 1112
DB 1155 AACTTACTACTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1214
QY 1113 AGCTACTGTATTTGTTGATGTGCCATATCATACTACCACTGTTTACAGTGAATGGAC 1172
DB 1215 TACTACTACTACTACTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1274
QY 1173 AGGAACAATCATACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1219
DB 1275 AACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1321
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 8, 2005, 17:41:17 ; Search time 202 Seconds

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Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 3548624

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Database : Published Applications AA:*

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17: /cgm2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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1	2174	94.6	1260	14	US-10-245-802-8	Sequence 8, Appli
2	1885	82.1	1119	14	US-10-245-802-12	Sequence 12, Appli
3	1865	81.2	1270	14	US-10-245-802-16	Sequence 16, Appli
4	1832	79.8	1047	14	US-10-245-802-22	Sequence 22, Appli
5	1769.5	77.0	468	14	US-10-245-802-10	Sequence 10, Appli
6	1596	69.5	469	14	US-10-245-802-14	Sequence 14, Appli
7	1544.5	67.2	468	14	US-10-245-802-24	Sequence 24, Appli
8	1500	65.3	1443	14	US-10-245-802-18	Sequence 18, Appli
9	961.5	41.9	2297	14	US-10-245-802-20	Sequence 20, Appli
10	308.5	13.4	650	15	US-10-369-493-22177	Sequence 22177, A
11	179	7.8	800	14	US-10-029-386-32198	Sequence 32198, A
12	177	7.7	1322	9	US-09-801-368-114	Sequence 114, App
13	177	7.7	1322	15	US-10-369-493-1353	Sequence 1353, Ap
14	177	7.7	1537	9	US-09-801-368-104	Sequence 104, App
15	177	7.7	1537	15	US-10-369-493-1398	Sequence 1398, Ap
16	177	7.7	1537	17	US-10-324-035-17	Sequence 17, Appli
17	172	7.5	1217	16	US-10-734-564-122	Sequence 122, App
18	170	7.4	957	10	US-09-840-746-19	Sequence 19, Appli
19	165.5	7.2	4262	17	US-10-704-781-4	Sequence 4, Appli
20	165.5	7.2	4493	17	US-10-704-781-3	Sequence 3, Appli
21	161.5	7.0	1075	9	US-09-801-368-110	Sequence 110, Appli
22	161.5	7.0	1075	15	US-10-369-493-22068	Sequence 22068, A
23	156	6.8	688	9	US-09-864-761-36047	Sequence 36047, A
24	154.5	6.7	1367	9	US-09-801-368-108	Sequence 108, App
25	154	6.7	1283	15	US-10-369-493-22616	Sequence 22616, A
26	151.5	6.6	1797	15	US-10-369-493-5176	Sequence 5176, Ap
27	151.5	6.6	1805	15	US-10-369-493-5177	Sequence 5177, Ap
28	150.5	6.6	288	9	US-09-216-393-341	Sequence 341, App
29	150.5	6.6	288	9	US-09-216-393-344	Sequence 344, App
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32	150.5	6.6	725	15	US-10-369-493-2004	Sequence 2004, App
33	150	6.5	386	9	US-09-864-761-35720	Sequence 35720, A
34	149.5	6.5	2139	17	US-10-480-456-1	Sequence 1, Appli
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36	146.5	6.4	1169	15	US-10-369-493-22288	Sequence 22288, A
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39	145	6.3	1041	15	US-10-369-493-1935	Sequence 1935, Ap
40	145	6.3	1609	15	US-10-369-493-1535	Sequence 1535, Ap
41	145	6.3	2435	15	US-10-282-122A-47453	Sequence 47453, A
42	144.5	6.3	609	15	US-10-369-493-22725	Sequence 22725, A
43	144.5	6.3	609	15	US-10-369-493-22806	Sequence 22806, A
44	144.5	6.3	3930	15	US-10-282-122A-46817	Sequence 46817, A
45	143	6.2	550	15	US-10-369-493-10236	Sequence 10236, A

ALIGNMENTS

RESULT 1
; Sequence 8, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1260
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-8

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Pred. No.: 1.16e-189 Length: 1260
Score: 2174.00 Matches: 413
Percent Similarity: 99.52% Conservative: 0
Best Local Similarity: 99.52% Mismatches: 2
Query Match: 94.65% Indels: 0
DB: 14 Gaps: 0

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DB 38 TyrAlaPheLysGlyProGlyTyrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57
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DB 98 PheTyrSerGlyGluGluPheThrThrPheSerThrLeuThrCysThrValAsnAspAla 117
QY 301 TTGAAATCATCCATTAAGGATTTGGTACAGTACTTTTACCAATGTCATTCAATGTTGGT 360
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RESULT 2

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US-10-245-802-12
; Sequence 12, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 1119
; TYPE: PR1
; ORGANISM: Candida albicans
US-10-245-802-12
```

Alignment Scores:

Pred. No.: 3.07e-163 Length: 1119
Score: 1885.00 Matches: 352
Percent Similarity: 92.05% Conservative: 30
Best Local Similarity: 84.82% Mismatches: 33
Query Match: 82.06% Indels: 0
DB: 14 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-12 (1-1119)

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QY 1 AAGACATCACTGCTGTTTGTAGTAAATCAATTAATCAATGGTCCAAATGCTGCTAAAT 60
DB 18 LysThrIleThrGlyValPheAsnSerPheAsnSerLeuThrTrpSerAsnAlaAlaThr 37
QY 61 TATGCTTTCAAAGGCCAGGATACCCAACTGGAAATGCTGTTTGGTGGTTCCTTAGAT 120
DB 38 TyrAsnTyrLysGlyProGlyThrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57
QY 121 GGTACCAAGTCCCAATCCAGGGGATACATTCACATTGAATATGCTGCTGTTTAAATAT 180
DB 58 GlyThrSerAlaSerProGlyAspThrPheThrLeuAsnMetProCysValPheLysPhe 77
QY 181 ACTACTTCAAAACATCTGTTGATTTAACTGCCGATGGTGTGTTAAATATGCTACTGTCAA 240
DB 78 ThrThrSerGlnThrSerValAspLeuThrAlaHisGlyValLysTyrAlaThrCysGln 97
QY 241 TTTTATCTGGTGAAGAATTCACAACTTTTCTACATTAACTGATGCTGTAACGACGCT 300
DB 98 PheGlnAlaGlyGluGluPheMetThrPheSerThrLeuThrCysThrValSerAsnThr 117
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Db 418 ThrAenProThrAspSerIleAspThrValIleValGlnValPro 432

RESULT 5

US-10-245-802-10

; Sequence 10, Application US/10245802

; Publication No. US20030124134A1

; GENERAL INFORMATION:

; APPLICANT: Edwards, John E.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST

; FILE REFERENCE: 013361.4003

; CURRENT APPLICATION NUMBER: US/10/245,802

; CURRENT FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: US 09/715,876

; PRIOR FILING DATE: 2000-11-18

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 10

; LENGTH: 468

; TYPE: PRT

; ORGANISM: Candida albicans

US-10-245-802-10

Alignment Scores:

Pred. No.:	8,72e-153	Length:	468
Score:	1769.50	Matches:	333
Percent Similarity:	86.75%	Conservative:	27
Best Local Similarity:	80.24%	Mismatches:	54
Query Match:	77.04%	Indels:	1
DB:	14	Gaps:	1

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-10 (1-468)

Qy 1 AAGACAATCAGCTGGGTTTTCATAGTTTAAATTCATTAACTGGTCCAAAGCTGCTCAAT 60

Db 18 LysValIleThrGlyValPheAsnSerPheAspSerLeuThrTrpThrArgAlaGlyAsn 37

Qy 61 TATGCTTTCAAGGCCAGGATACCCAACTTGGAAATGCTGTTTGGGTTGGTCCCTTAGAT 120

Db 38 TyrAlaIleThrGlyProAsnArgProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57

Qy 121 GGTACAGTGCACATCCAGGGGATACATTCAATTCATTAATGCCATGTGTGTTAAATPAT 180

Db 58 GlyThrSerAlaAsnProGlyAspThrPheThrLeuAsnMetProCysValPheIleAspPhe 77

Qy 181 ACTACTTCACAAACATCTGTTGATTAACGCGATGTTTAAATGCTGCTACTGTTCAAA 240

Db 78 IleThrAspGlnThrSerValAspLeuThrAlaGluGlyValLysThrAlaThrCysGln 97

Qy 241 TTTTATCTGGTGAAGATTCCAACTTTTCTACATTAAACATGACTGTGAACGACGCT 300

Db 98 PheTyrSerGlyGluGluPheThrThrPheSerSerLeuLysCysThrValSerAsnThr 117

Qy 301 TTGAATCATCATTAAGSCATTTGCTGACAGTTACTTTTACCAATTCGATTCATTAATGTTGCT 360

Db 118 LeuThrSerSerIleLysAlaLeuGlyThrValThrLeuProIleSerPheAsnValGly 137

Qy 361 GGAAACAGTTTCATCACTGATTTGGAAGATTCTAAATGTTTACTGCTGGTACCAATACA 420

Db 138 GlyThrGlySerSerValAspLeuGluSerSerGlnCysPheLysAlaGlyThrAsnThr 157

Qy 421 GTCACATTTAATGATGCTGAATAAGATATCTCAATGATGTTGAGTTTGAAAGTCAACC 480

Db 158 ValThrPheAsnAspGlyAspLysLysIleSerIleAspValAspPheGluLysThrAsn 177

Qy 481 GTTGATCCAAAGTGCATATTGTTATGCTTCCAGATTATGCCAAGTCTCAATAAGTGCACA 540

Db 178 GluAspAlaSerGlyTyrPheIleAlaSerArgLeuIleProSerIleAsnLysValSer 197

Qy 541 ACTCTTTTGTGGCCACCAATGTGAAATGTTTACATCTGGTACAAATGGGTTCTCC 600

Db 198 IleThrTyrValAlaProGlnCysAlaAsnGlyTyrThrSerGlyAlaMetGlyPheIle 217

Qy 601 AGTAGTAACGGTGACGTTGCTATTGATTGCTCAAAATATTCATATTGTTGATATCACAAGGA 660

Db 218 ValLeuThrGlyAspThrThrIleAspCysSerAsnValHisValGlyIleThrLysGly 237

Qy 661 TTAATGATTTGGAATTAATCGGTTTTCATCTGAATCATTTAGTTACACTAAACCTTGTACA 720

Db 238 LeuAsnAspTrpAsnPheProValSerSerAspSerLeuSerIleAsnLysThrCysSer 257

Qy 721 TCTAATCGAATTCAGATTAAATATCAAAATGTACTGCTGCTGTTATCTGCTCAATTTATTGAT 780

Db 258 SerThrGlyIleSerIleThrTyrGluAsnValProAlaGlyTyrArgProPhePheAsp 277

Qy 781 GCTTATATTCTGCTACAGATGTTAACAAATATATCTTTAGCATATATACAAATGATTACT 840

Db 278 ValTyrThrSerValSerGlyGlnAsnArg---GlnLeuArgTyrThrAsnAspTyrAla 296

Qy 841 TGTCTGGCAGTCTGCTGCAAGTAAACCTTTCACTTTAAGATGAGTGGATACAGAAT 900

Db 297 CysValGlySerSerLeuGlnSerLysPheAsnLeuArgLeuArgGlyTyrAsnAsn 316

Qy 901 AGTGATCCGGATCTAAACGGTATTGTTCAATGTTGCTTACAACTAGAACAGTTTACAGACAGT 960

Db 317 SerGluAlaAsnSerAsnGlyPheValIleValAlaThrAlaThrValThrAspSer 336

Qy 961 ACCACTGCTGCTACTACTTTTACCATTCATCCAAAGTGTGTGATAAAACCAAAATCAATCAA 1020

Db 337 ThrThrAlaValThrThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu 356

Qy 1021 ATTTTGCACTTATCCAACTTACCATTCACATTCACATTCATATGTTGGTGTGACTACTTCC 1080

Db 357 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 376

Qy 1081 TATCTGACTGAAGTCTGACCAATTTGTTGAAACAGTACTGTTATTGTTGATGTCCTCAT 1140

Db 377 TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 396

Qy 1141 CATACTACCAACTGTTTACAGTGAATGAGACAGAGAAACATCATCTACCAACCACTCGT 1200

Db 397 HisThrThrThrValThrValThrSerGluTrpThrGlyThrIleThrThrThrThrArg 416

Qy 1201 ACCAATCCAACTGATTCATTTGACACAGTGGTGGTACAGTTCCA 1245

Db 417 ThrAsnProThrAspSerIleAspThrValValGlnValPro 431

RESULT 6

US-10-245-802-14

; Sequence 14, Application US/10245802

; Publication No. US20030124134A1

; GENERAL INFORMATION:

; APPLICANT: Edwards, John E.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST

; FILE REFERENCE: 013361.4003

; CURRENT APPLICATION NUMBER: US/10/245,802

; CURRENT FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: US 09/715,876

; PRIOR FILING DATE: 2000-11-18

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 14

; LENGTH: 469

; TYPE: PRT

; ORGANISM: Candida albicans

US-10-245-802-14

Alignment Scores:

Pred. No.:	6.48e-137	Length:	469
Score:	1596.00	Matches:	295
Percent Similarity:	81.20%	Conservative:	42
Best Local Similarity:	71.08%	Mismatches:	78
Query Match:	69.48%	Indels:	0
DB:	14	Gaps:	0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-14 (1-469)

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QY 1 AAGCAATCACTGGTGGTTTGTAGTAAATTCATTAACTGGTCCCAATGCTGCTAAT 60
Db 18 LysValIleThrGlyValPheAsnSerPheAsnSerLeuThrTrpAlaAsnAlaLaser 37
QY 61 TATGCTTTCAAAGGCCAGGATACCCAACTTGGAATGCTGTTTGGGTTGGTCTTAGAT 120
Db 38 TyrProTyrArgGlyProAlaThrProThrTrpThrAlaValIleGlyTrpSerLeuAsp 57
QY 121 GGTACCAAGTCCAAATCCAGGGATACATTCACATTTGAATATGCCATGTGTGTTAAATAT 180
Db 58 GlyAlaThrAlaLaserAlaGlyAspThrPheThrLeuAspMetProCysValPheLysPhe 77
QY 181 ACTACTTTCACAAACATCTGTTGATTTAACTGCGATGGTGTAAATATGCTACTGTGCAA 240
Db 78 IleThrAspGlnThrSerIleAspLeuValAlaAspGlyArgThrTyrAlaThrCysAsn 97
QY 241 TTTTATTCTGCTGAAGAAATTCACAACTTTTCTACATTAACATGCTGTGAACAGCT 300
Db 98 LeuAsnSerAlaGluGluPheThrThrPheSerSerValSerCysThrValThrThrThr 117
QY 301 TTGAATATCATCAATTAAGCAATTTGGTACAGTTACTTTTACCAATGTCATCAATGTTGCT 360
Db 118 MetThrAlaAspThrLysAlaIleGlyThrValThrLeuProPheSerPheSerValGly 137
QY 361 GGAACAGTTTCATCACTGTTGGAAGATTCCTAAATGTTTACTGCTGTGTACCAATACA 420
Db 138 GlySerGlySerAspValAspLeuAlaAsnSerGlnCysPheThrAlaGlyIleAsnThr 157
QY 421 GTCACTTTTAAATGATGGTGAATAAGATATCTCAATGATGTTGAGTTGAAAAGTCAACC 480
Db 158 ValThrPheAsnAspGlyAspThrSerIleSerThrThrValAlaAspPheGluLysSerThr 177
QY 481 GTTGATCCAGTGATATTTGTATGCTTCCAGATTAATGCCAGTTCATATAGGTGACA 540
Db 178 ValAlaSerSerAspArgIleLeuLeuSerArgIleLeuProSerLeuSerGlnAlaVal 197
QY 541 ACTCTTTTGTGGCCACCAATGGAATGTTTACACATCTGTCAATGGAATGGGTTCTCC 600
Db 198 AsnLeuPheLeuProGlnGluCysAlaAsnGlyTyrThrSerGlyThrMetGlyPheSer 217
QY 601 AGTAGTAACGGTGAAGTTGCTTATTGATTCCTCAATATTCATATGCTATGCTATCAAAAAGGA 660
Db 218 ThrAlaGlyThrGlyAlaThrIleAspCysSerThrValHisValGlyIleSerAsnGly 237
QY 661 TTAATGATTTGGAATATTCGGTTTCATCTGAATCATTTAGTTACATTAACAACTGTACA 720
Db 238 LeuAsnAspTrpAsnTyrProIleSerSerGluSerPheSerTyrThrLysThrCysThr 257
QY 721 TCTAATGGAATTCAGATTAATATCAAAATGCTACTGCTGTTATCGTTCATTTATTGAT 780
Db 258 SerThrSerValLeuValThrPheGlnAsnValProAlaGlyTyrArgProPheValAsp 277
QY 781 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTAGCATATACCAATGATTAFACT 840
Db 278 AlaTyrIleSerAlaThrArgValSerSerTyrThrMetGlnTyrThrAsnIleTyrAla 297
QY 841 TGCTGTCAGTCTGTCGAAGTAAACCTTTTCATTTAGATGGAATGGAATGATCAAGAT 900
Db 298 CysValGlyAlaAlaSerValAspAspSerPheThrHisThrTrpArgGlyTyrSerAsn 317
QY 901 AGTCATGCGGATCTAAGCGTATTTGCTATGCTCAACCTAGAACAGATTCACAGACGT 960
Db 318 SerGlnAlaGlySerAsnGlyIleThrIleValValThrThrArgThrValThrAspSer 337
QY 961 ACCACTGCTGCTACTACTTTTACCAATCAATCAAGTGTGTATAAAACCAAAACATGCAA 1020
Db 338 ThrThrAlaValThrThrLeuProPheAsnSerAspThrAspLysThrLysThrIleGlu 357
QY 1021 ATTTTGCACCTATTCACACCACTTACCATCTCATATGTTGGTGGTCACTCTCC 1080
Db 358 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 377
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QY 1081 TATCTGACTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATTGTTGATGTCATAT 1140
Db 378 TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 397
QY 1141 CATACTACCAACACTGTTTACCAGTGAATGACAGGACAAATCACTACCAACCACTCGT 1200
Db 398 HisThrThrThrThrValThrSerGluTrpThrGlyThrIleThrThrThrThrArg 417
QY 1201 ACCAATCCAACTGATTCAATTCACACAGTGGTGGTCAAGTTCCA 1245
Db 418 ThrAsnProThrAspSerIleAspThrValValValGlnValPro 432
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RESULT 7

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US-10-245-802-24
; Sequence 24, Application US/10245802
; Publication No. US20030124134A1
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GENERAL INFORMATION:

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; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-24
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Alignment Scores:

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Pred. No.: 3,33e-132 Length: 468
Score: 1544.50 Matches: 291
Percent Similarity: 83.13% Conservative: 54
Best Local Similarity: 70.12% Mismatches: 69
Query Match: 67.24% Indels: 1
DB: 14 Gaps: 1
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US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-24 (1-468)

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QY 1 AAGCAATCACTGGTGGTTTGTAGTAAATTCATTAACTGGTCCCAATGCTGCTAAT 60
Db 18 LysThrIleThrGlyValPheAsnSerPheAspSerLeuThrTyrThrArgSerValGlu 37
QY 61 TATGCTTTCAAAGGCCAGGATACCCAACTTGGAATGCTGTTTGGGTTGGTCTTAGAT 120
Db 38 TyrAlaTyrLysGlyProGluThrProThrTyrAsnAlaValLeuGlyTyrSerLeuAsn 57
QY 121 GGTACCAAGTCCAAATCCAGGGATACATTCACATTTGAATATGCTATGCTGTTAAATAT 180
Db 58 SerThrThrAlaAspProGlyAspThrPheThrLeuIleLeuProCysValPheLysPhe 77
QY 181 ACTACTTTCACAAACATCTGTTGATTTTAACTGCGATGGTGTAAATATGCTACTGTGCAA 240
Db 78 IleThrThrGlnThrSerValAspLeuThrAlaAspGlyValSerTyrAlaThrCysAsp 97
QY 241 TTTTATTCTGCTGAAGAAATTCACAACTTTTCTACATTAACATGCTACTGTAACGACGCT 300
Db 98 PheAsnAlaGlyGluGluPheThrThrPheSerSerLeuSerCysThrValAsnSerVal 117
QY 301 TTGAATATCATCAATTAAGCAATTTGGTACAGTTACTTTTACCAATGTCATTTCAATGTTGCT 360
Db 118 SerValSerTyrAlaArgValSerGlyThrValLysLeuProIleThrPheAsnValGly 137
QY 361 GGAACAGTTTCATCACTGTTGGAAGATTCCTAAATGTTTACTGCTGGTACCAATACA 420
Db 138 GlyThrGlySerSerValAspLeuAlaAspSerLysCysPheThrAlaGlyLysAsnThr 157
QY 421 GTCACTTTTAAATGATGGTGAATAAGATATCTCAATGATGTTGAGTTGAAAAGTCAACC 480
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QY 895 AAGAATAGTGCATCGGATCTAACGGTATTGTTCATTGTTGCTACAACTAGACAGTTTACA 954
Db 319 ThrAsnSerAspAlaGlySerAsnGlyAlaValValValThrThrArgThrValThr 338
QY 955 GACAGTACCCTGCTGTCATCTTACCATTCAATCAAGTGTGTGATAAACCACCAACA 1014
Db 339 AspSerThrAlaIleThrThrLeuProPheAspProThrValAspLysThrLysThr 358
QY 1015 ATCGAAATTTGCAACCTATTCCCAACCACTACCACTCAACCTCATATGTTGGTGCACT 1074
Db 359 IleGluValIleGluProIleProThrThrThrIleThrThrSerTyrValGlyIleSer 378
QY 1075 ACTTCCTATCTGCTAAGACTGCACCAATTTGGTGAACAGCACTACTGTTATTGTTGATGTG 1134
Db 379 ThrSerLeuSerThrLysThrAlaThrIleGlyGlyThrAlaThrValValValAspVal 398
QY 1135 CCATATCATCTACACAACTGTTTACCAGTGAATGGACAGAACATCACTACCAACACA 1194
Db 399 ProTyrHisThrThrThrIleThrSerIleTyrThrGlySerAlaThrThrSerSer 418
QY 1195 ACTCGTACCACCACTGATTCAATTCAGACAGTGGTGTTACAAAGTTCCA 1245
Db 419 ThrTyrThrAsnProThrAspSerIleAspThrValValGluValPro 435

RESULT 9
US-10-245-802-20
; Sequence 20: Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 2297
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-20

Alignment Scores:
Pred. No.: 1,14e-78 Length: 2297
Score: 961.50 Matches: 192
Percent Similarity: 63.94% Conservative: 74
Best Local Similarity: 46.15% Mismatches: 149
Query Match: 41.86% Indels: 1
DB: 14 Gaps: 1

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-245-802-20 (1-2297)
QY 1 AAGCAATCACTGGTGTGTTTGTAGATTTTAAATTCATTAACTTGGTCCAATGCTGCTAAT 60
Db 19 LysGluValThrGlyValPheAsnGluPheAsnSerLeuIleTyrSerTyrThrTyrArg 38
QY 61 TATGCTTTCAAGGCCAGGATACCACCACTTGGAAATGCTGTTGGTGGTGGTCTTAGAT 120
Db 39 AlaArgTyrGluGluIleSerThrLeuThrAlaAsnAlaGluLeuGluTyrAlaLeuAsp 58
QY 121 GGTACCACTGCAATCCAGGGGATACATTCATTTGAATGCAATGCTGTTGTTTAAATAT 180
Db 59 GlyThrIleAlaSerProGlyAspThrPheThrLeuValMetProCysValTyrLysPhe 78
QY 181 ACTACTTCACAAACATCTGTTGATTAACTCCGCGATGGTGTAAATATGCTACTTGTCAA 240
Db 79 MetThrTyrGluThrSerValGluLeuThrAlaAsnSerIleAlaTyrAlaThrCysAsp 98
QY 241 TTTTATCTGTTGGAAGATTCACAACTTTCTACATTAACATGCTACTGTGAACGACGCT 300
Db 119 PheAspAlaGlyGluAspThrLysSerPheSerSerLeuLysCysThrValThrAspGlu 118
QY 301 TTCAAAATCATCCATTAAAGCATTTGGTACAGTTTACTTTTACCAATTCATTCAATGTTGGT 360
Db 119 LeuThrGluAspThrSerValPheGlySerValIleLeuProIleAlaPheAsnValGly 138
QY 361 GGAACAGGTTCATCAACTGATTGGGAAGATTCCTAAATGTTTACTCTGCTGGTACCAATACA 420
Db 139 GlySerGlySerLysSerThrIleThrAspSerLysCysPheSerSerGlyTyrAsnThr 158
QY 421 GTACACATTTAATAGTCGTGATAAAGATATCTCAATTTGATGTTGAGTTTCAAAAGTCAACC 480
Db 159 ValThrPhePheAspGlyAsnAsnGluLeuSerThrThrAlaAsnPheLeuProArgArg 178
QY 481 GTTGATCCCAAGTCATATTGTTATGCTTCACAGAGTTATGCCAAGTTCATCAATAGGTGCACA 540
Db 179 GluLeuAlaPheGlyLeuValValSerGluArgLeuSerMetSerLeuAspThrMetThr 198
QY 541 ACTCTTTTGTGGCCACCAACATGTTGAANAATGGTTACACATCTGGTACAAATGGGGTCTCC 600
Db 199 AsnPheValMetSerThrProCysPheMetGlyTyrGlnSerGlyLysLeuGlyPheThr 218
QY 601 AGTAGTAACGGTGACGTTGCTATTGATTGCTCAAAATATTCATATTGATTCACAAAGGA 660
Db 219 SerAsnAspAspPheGluIleAspCysSerSerIleHisValGlyIleThrAsnGlu 238
QY 661 TTAATGATTGGAATTTATCCGGTTTCATCTGAATCATTTAGTTTACATAAACTTGTACA 720
Db 239 IleAsnAspTyrSerMetProValSerSerValProPheAspHisThrIleArgCysThr 258
QY 721 TCTAATGGAATTCAGATTAAATATCAAAATGATCTGCTGGTGGTATCGTCCATTTATGAT 780
Db 259 SerArgAlaLeuTyrIleGluPheLysThrIleProAlaGlyTyrArgProPheValAsp 278
QY 781 GCTTATATTCTGCTACAGATGTTAACCATAATATCTTTAGCATATACCATGATGATTACT 840
Db 279 AlaIleValGluIleProThrThrGluProPheValLysTyrThrAsnGluPheAla 298
QY 841 TGTGCTGGCAGTCTGCTGCAAGATAAACCTTTTACCTTTTAAAGATGGACT---GGATACAAG 897
Db 299 CysValAsnGlyIleTyrThrSerIleProPheThrSerPhePheSerGlnProIleLeu 318
QY 898 AATAGTGATGCCGATCTAACGGTATTGTCATTGTTGCTACAACTAGACAGTTCAGAC 957
Db 319 TyrAspGluAlaLeuAlaIleGlyAlaAspLeuValArgThrThrSerThrValIleGly 338
QY 958 AGTACCACCTGCTGCTCACTACTTTTACCATTCAATCCCAAGTGTTCATAAAACCAAAACAATC 1017
Db 339 SerIleThrArgThrThrThrLeuProPheIleSerArgLeuGluLysThrLysThrIle 358
QY 1018 GAAATTTTGCACACTATTCCAACTACCACTACCACTTCAATTCATATGTTGGTGTGACTACT 1077
Db 359 LeuValLeuGluProIleProThrThrValThrThrSerHisGlyPheAspThr 378
QY 1078 TCCTATCTGACTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATTGTTGATGTCACA 1137
Db 379 TyrTyrTyrThrLysLysAlaThrIleGlyAspThrAlaThrValPheIleAspValPro 398
QY 1138 TATCATCTACCACTGTTTACCAGTGAATGACAGGACCAATCACTACCAACCAACAAT 1197
Db 399 GlnHisThrAlaThrThrLeuThrThrTyrTyrGlnGluSerSerThrAlaThrThr 418
QY 1198 CGTACCACTCAACTGATTCAATTTGACAGCTGGTGTCAAGTTCCA 1245
Db 419 TyrPheAspAspIleAspLeuValAspThrValIleValLysIlePro 434

RESULT 10
US-10-369-493-22177
; Sequence 22177, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
```

```

; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22177
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22177

Alignment Scores:
Pred. No.: 4,26e-19 Length: 650
Score: 308.50 Matches: 116
Percent Similarity: 43.33% Conservative: 79
Best local Similarity: 25.78% Mismatches: 190
Query Match: 13.43% Indels: 65
DB: 15 Gaps: 20

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-369-493-22177 (1-650)
QY 25 AGTTTAAATCAATTAATGTCCTCAAT-----GCTGCTAATATGCT 66
DB 21 AenileAenAspIleThrPheSerAenLeuGlulieThrProLeuThrAlaAen----- 38
QY 67 TTCAAAGGCGCAGGATACCCAACTTGGAACTGCTGTTTGGGTGTGCTCTTA---GATGGT 123
DB 39 ---LysGlnProAsp---GlnGlyTrpThrAlaThrPheAspPheSerilealaAspAla 56
QY 124 ACCAGTGCATCCAGGCGGATACATTCATTAATGATGCCATGTGTGTTTAAA----- 177
DB 57 SerSerileArgGluGluAspGluPheThrLeuSerMetProHieValTyrArgileLys 76
QY 178 ---TATACTACTTCAACAACATCTGTTGATTAATCACTGCGATGGTGAATATGCTACT 234
DB 77 LeuLeuAenSerSerGlnThrAlaThrileSerLeuAlaAepGlyThrGluAlaPheLys 96
QY 235 TGTCAATTTTATCTCGTGAA-----GAATCACAACCTTTTCTACATTA 279
DB 97 Cys---TyrValSerGlnGlnAlaAlaTyrLeuTyrGluAenThrThrPhe----- 112
QY 280 ACATGCTACTGTGAACGAGCTTTGAAATCATCCATTAAGGCATTTGGTACAGTTACTTTA 339
DB 113 ThrCysThrAlaGlnAenAspLeuSerSerTyrAenThrileAspGlySerileThrPhe 132
QY 340 CCAATTCATCAATGTTGGTGGAAACAGGTTTCATCACTGATTTGGAAGATCTTAAATGT 399
DB 133 SerLeuAenPheSerAspGlyGlySerTyrGluTyrGluLeuGluAenAlaLysPhe 152
QY 400 TTTACTGCTGGTACCAATACAGTCACATTTAATGATGGTGAATAAGATATCTCAATTGAT 459
DB 153 PheLysSerGlyProMetLeuValLysLeuGluYasnGlnMetSerAspVal----- 169
QY 460 GTTGTAGTTGAAAAGTCAACCCGTTGATCCAAGTCATAT-----TTGTATGCTTCC 510
DB 170 ValAenPhe-----AspProAlaAlaPheThrGluAenValPheHieSer 184
QY 511 AGAGTTATGCCAAGTCTCAATAGGTCAACAATCTTTTGTGGCCACCAATGTCAAAAT 570
DB 185 GlyArgSerThrGlyTyrGlySerPheGluSerTyrHieLeuGlyMetTyrCysProAen 204
QY 571 GGTTCACATCTGGT-----ACAATGGGTTCTCCAGTAGTAAGCGTGACCTGCT 621
DB 205 GlyTyrPheLeuGlyGlyThrGluLysIleAspTyrAspSerSerAenAenValAsp 224
QY 622 ATTGATTGCTCAAAATATTCATATTGATATCACAAAGGATTAATGATTGAATATCCG 681

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225 LeuAspCysSerSerValGlnValTyrSerSerAenAspPheAenAspTrpTrpPhePro 244
682 GTTTTCATCTCAATCATTTAGTACATAAACTTTGTACATCAATCAATGAATTCAGATTA 741
245 GlnSerTyrAenAspThrAenAlaAapValThrCysPheGlySerAenLeuTrpIleThr 264
742 TAT---CAAAATGTACTGCTGCTGTTATCGTCCATTTATTTGATGCTATATTTCT---GCT 795
265 LeuAspGluLysLeuTyrAspGlyGluMetLeuTrpValAenAlaLeuGlnSerLeuPro 284
796 ACAGATGTTTAAACCAATATATCTTTAGCATATACCAATGATTTATATCTCT--- 843
285 AlaAenValAenThrileAspHieAlaLeuGluPheGlnTyrCysLeuAspThrIle 304
844 GCTGGCAGTCTGCTGCAAAAGTAAACCTTTTCATCTTTTAAAG-----TGGACTGGA 891
305 AlaAenThrThrTyrAlaThrGlnPheSerThrThrArgGluPheIleValTyrGlnGly 324
892 TACAAGAAATAGTATGATCCGATCTTAACGGTATTTGTCATTTGTTGCTACAACTAGAACAGTT 951
325 ArgAenLeuGlyThrAlaSerAlaLysSerSerPheIleSerThrThrThrThrAspLeu 344
952 ACAGAC-----AGTACCACCTGCTGCTCACTACTTACCATTCAATCCA 993
345 ThrSerIleAenThrSerAlaTyrSerThrGlySerIleSerThrVal----- 360
994 AGTGTTCATAAAACCAAAACCAATTCGAAATTTTGCACCTATTCACCACTACCATCACA 1053
361 GluThrGlyAenArgThrThrSerGluValIleSerHieValValThrThrSerThrLys 380
1054 ACTTCATATGTTGGTGTGACTACTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113
381 LeuSerProThrAlaThrThrSerLeuThrileAlaGlnThrSerIleTyrSerThrAsp 400
1114 GCTACTGTTATTTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1152
401 SerAenIleThrValGlyThrAspIleHieThrThrSerGluValIleSerAspValGlu 420
1153 ACTGTTACCACTGATGAGACAGGAAACATCACTACCACTACCACTACCACTACCACTACCA 1209
421 ThrIleSerArgGluThrAlaSerThrValValAlaAlaProThrSerThrThrGlyTrp 440
1210 ACTGATTCAATTTGACACAGTGGTGGTACAA 1239
441 ThrGlyAlaMetAenThrTyrIleSerGln 450

RESULT 11
US-10-029-386-32198
; Sequence 32198, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32198
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007663.28
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3

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Db GluGlnProProlleThrSerThrAsnPhethrileAen-----Glyile 193
Qy 316 AAGCAATTT-----GGTACAGTT----- 333
Db LysProTrpAenglySerProProAspAsnleThrGlyThrValTyrMetTyrAlaGly 213
Qy 334 -----ACTTTACCAATTT 345
Db 214 PheTyrTyrProMetLysIleValTyrSerAsnAlaValAlaTrpGlyThrLeuProile 233
Qy 346 GCATTCATGTT---GGTGGACAGGTTTCATCACTGATTGGAGAGATTCTAAATGTTTT 402
Db 234 SerValThrLeuProAspGlyThrThrValSerAspPheGluGly----- 249
Qy 403 ACTGCTGTACCAATACAGTCACATTTAATGATGGTGTATAAGATATCTCAATTCATGTT 462
Db 250 -----TyrValTyrPhe-----AspAsnAsnLeuSer----- 259
Qy 463 GAGTTTGAAGAGTCACCGTTGATCCAGTGCATATTTGTTATGCTTCCAGAGTTATGCCA 522
Db 260 GlnProAsnCysThrIleProAspProSerAsnTyrThr-----ValSerThrThrIleThr 278
Qy 523 AGTCTCAATAAGGTCACAACTCTTTTGTGGCACCAACAATGTGAATGGTTACACATCT 582
Db 279 ThrThrGluProTTPThrGlyThrPheThrSerThrSerThrGluMetThrThrValThr 298
Qy 583 GGTACAATGGGTTCTCAGTAGTAACCGGTGACGTGTCTATTGATTGCTCAATATTCAT 642
Db 299 GlyThrAsnGlyValProThrAspGluThrValIleValIleAargThrProThrThrAla 318
Qy 643 ATTGGTATCAAAAGGATTAAATGATTGGAATTATCCGTTTCATCTGAATCATTTAGT 702
Db 319 SerThrIleIleThrThrGluProTrpAsnSerThrPheThrSerThrSerThrGlu 338
Qy 703 TACATAAACTGTGTACATCTAATGGAATTCAGATTAATAATCAAAATGTACCTCGT 762
Db 339 LeuthrThrValThrGlyThrAsnGlyValargThrAspGluThrIleIle----- 355
Qy 763 TATGCTCATTTATTGATGCTTATATTTCTGTCAGATGTTAACCAATATACCTTTAGCA 822
Db 356 -----ValIleAargThrProThrThrAlaThrThrAlaIleThrThrGluPro 372
Qy 823 TATACCAATGATTATCTGCTGGCAGTGTCTGCAAGTGTCTGCAAGTAAACCTTTCACTTAAGA 882
Db 373 TrpAsnSerThrPheThrSerThrSerThrGluLeu----- 384
Qy 883 TGGACTGTGATCAAGAAATAGTGCATCGCGATCTAACGGTATT-----GTCATTTGTT 933
Db 385 -----ThrThrValThrGlyThrAsnGlyLeuProThrAspGluThrile 399
Qy 934 GCTACAACACTAGAACAGTTACAGACAGTACCACTGCTGTCTACTTTA-----CCATTCAT 990
Db 400 IleValIleAargThrProThrThrAlaThrThrAlaMetThrThrThrGlnProTrpAsn 419
Qy 991 CCAAGTGTGTAAACCAACA----- 1014
Db 420 AspThrPheThrSerThrSerThrGluLeuthrThrValThrGlyThrAsnGlyLeuPro 439
Qy 1015 -----ATCGAATTTTGCACCTATTCCAACCACTATCCACTACCATCACAACT--- 1056
Db 440 ThrAspGluThrIleIleValIleAargThrProThrThrAlaThrThrAlaMetThrThr 459
Qy 1057 -----TCATANGTGGTGTGACTACTTCTCTATCTGACTCAAGAGTCA 1098
Db 460 ThrGlnProTTPAsnAspThrPheThrSerThrSerThrGluLeuthrThrValThrGly 479
Qy 1099 -----CCATTTGGTGAACAGTACTGTTATTGTTGATGTGGCCATATCACT 1146
Db 480 ThrAsnGlyLeuProThrAspGluThr-----IleIleValIleAargThrProThrThrAla 498
Qy 1147 ACCACA-----ACTGTTACCAAGTGAATGGACAGGAACAATCACT----- 1185
Db 499 ThrThrAlaMetThrThrGlnProTrpAsnAspThrPheThrSerThrSerThrGlu 518

Qy 1186 ---ACCACCAAACTCGTACCAAT-----CCAACTGATTCAATTGACACAGTGGTGTGA 1236
Db 519 IleThrThrValThrGlyThrAsnGlyLeuProThrAsp-----GluThrIleIleVal 536
RESULT 13
US-10-369-493-1353
; Sequence 1353, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1353
; LENGTH: 1322
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1353
Alignment Scores:
Pred. No.: 5,61e-07 Length: 1322
Score: 177.00 Matches: 112
Percent Similarity: 34.38% Conservative: 53
Best Local Similarity: 23.33% Mismatches: 181
Query Match: 7.71% Indels: 134
DB: 15 Gaps: 26

US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-369-493-1353 (1-1322)
Qy 58 AATTATGCTTTCAAGGCCAGGATACCCAACTGGATGCTGTTTGGGT---TGGTCC 114
Db 104 AsnTrpGlyCysLysGlyIleGlyAlaCysSerAsnAsnProIleIleAlaTyrTrpSer 123
Qy 115 TTAGAT-----GTACCAGTGCACATCCAGGGATACATTCACATTCGAATATG----- 162
Db 124 ThrAspLeuPheGlyPheTyrThrThrProThrAsnVal---ThrLeuGluMetThrGly 142
Qy 163 -----CCATGTGTGTTAAATATATATCTACTTCACAAACATCT 198
Db 143 TyrPheLeuProGlnThrGlySerTyrThrPheLysPheAlaThrValAspAspSer 162
Qy 199 GTTGATTAACTGCCGATGTT---GTTAAATATGCTACTTGTCAATTTTATTCTGGTGAA 255
Db 163 AlaIleLeuSerValGlyGlySerIleAlaPheGluCysCys-----AlaGln 178
Qy 256 GAATTCACAACTTTTTCATACATTAACTGCTGAACGACGCTTTGAAATCATCATCT 315
Db 179 GluGlnProProlleThrSerThrAsnPhethrileAen-----Glyile 193
Qy 316 AAGCAATTT-----GGTACAGTT----- 333
Db 194 LysProTrpAenglySerProProAspAsnIleThrGlyThrValTyrMetTyrAlaGly 213
Qy 334 -----ACTTTACCAATTT 345
Db 214 PheTyrTyrProMetLysIleValTyrSerAsnAlaValAlaTrpGlyThrLeuProile 233
Qy 346 GCATTCATGTT---GGTGGACAGGTTTCATCACTGATTGGAGAGATTCTAAATGTTTT 402
Db 234 SerValThrLeuProAspGlyThrThrValSerAspPheGluGly----- 249
Qy 403 ACTGCTGTGATCAATACAGTCACATTTAATGATGGTGTATAAGATATCTCAATTCATGTT 462

Db 250 -----TyrValTyrThrPhe-----AspAsnAsnLeuSer----- 259
Qy 463 GAGTTTGAAAGTCAACCGTTGATCCAAAGTGCATATTTGTATGCTTCCAGAGTTATGCCA 522
Db 260 GlnProAsnCysThrIleProAspProSerAsnTyrThr---ValSerThrThrIleThr 278
Qy 523 AGTCTCAATAAGGTCAACAACCTCTTTTGTGGCCACCAAAATGTGGAATGGTTACACATCT 582
Db 279 ThrGluProIleThrGlyThrPheThrSerThrGluMetThrThrValThr 298
Qy 583 GGTACAATGGGTTCTCCAGTAGTAACGGTGCATGCTGCTATTCATTCGCTCAATATTCAT 642
Db 299 GlyThrAsnGlyValProThrAspGluThrValIleValIleArgThrProThrThrAla 318
Qy 643 ATTGGTATCACAAAGGATTAAATGATTCGAAATTCCTCGGTTTCATCTGAATCATTTAGT 702
Db 319 SerThrIleIleThrThrGluProIleProIleSerThrPheThrSerThrThrGlu 338
Qy 703 TACACTAAAACCTTGTACATCTAATGGAATTCAGATTAAATATCAAAATGACCTGCTGGT 762
Db 339 LeuThrThrValThrGlyThrAsnGlyValArgThrAspGluThrIleIle----- 355
Qy 763 TATGCTCCATTATGATGCTTATATTCCTGCTACAGATGTTAACCAATATATCTTTAGCA 822
Db 356 -----ValIleArgThrProThrThrAlaThrThrAlaIleThrThrGluPro 372
Qy 823 TATACCAATGATATATCTGCTGGCGAGTCGCTGCAAAAGTAAACCTTCACTTTAAGA 882
Db 373 TrpAsnSerThrPheThrSerThrSerThrGluLeu----- 384
Qy 883 TGGACTGGATACAGAATAGTATGTCGCGATCTAAACGGTATT-----GTCATGTT 933
Db 385 -----ThrThrValThrGlyThrAsnGlyLeuProThrAspGluThrIle 399
Qy 934 GCTACAACAGAGTGTACAGACAGTACACCTGCTGCTCACTTTA-----CAATTCAT 990
Db 400 IleValIleArgThrProThrThrAlaThrThrAlaMetThrThrGlnProIlePAsn 419
Qy 991 CCAAGTGTGTAACCAACCAACA----- 1014
Db 420 AspThrPheThrSerThrSerThrGluLeuThrThrValThrGlyThrAsnGlyLeuPro 439
Qy 1015 -----ATCGAAATTTGCAACCTATTCACCACTACCACTACCAACT--- 1056
Db 440 ThrAspGluThrIleIleValIleArgThrProThrThrAlaThrAlaMetThrThr 459
Qy 1057 -----TCATATGTTGGTGTGACTACTTCCTATCTGACTAAGACTGCA 1098
Db 460 ThrGlnProTrpAsnAspThrPheThrSerThrSerThrGluLeuThrThrValThrGly 479
Qy 1099 -----CCAATTTGGTGAACACAGTACTGTTATTTGATGTGCTATATCACT 1146
Db 480 ThrAsnGlyLeuProThrAspGluThr-----IleIleValIleArgThrProThrThrAla 498
Qy 1147 ACCACA-----ACTGTTACAGTGAATGGACAGAAACAATCACT----- 1185
Db 499 ThrThrAlaMetThrThrGlnProTrpAsnAspThrPheThrSerThrSerThrGlu 518
Qy 1186 ---ACCACCAACACTGTTACCAAT-----CCAACTGATTCAATTGACAGTGGTGTA 1236
Db 519 IleThrThrValThrGlyThrAsnGlyLeuProThrAsp-----GluThrIleIleVal 536

RESULT 14

US-09-801-368-104
; Sequence 104, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary

Alignment Scores:
Pred. No.: 5,86e-07 Length: 1537
Score: 177.00 Matches: 112
Percent Similarity: 32.72% Conservative: 47
Best Local Similarity: 23.05% Mismatches: 181
Query Match: 7,71% Indels: 146
DB: 25 Gaps: 25

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-801-368-104 (1-1537)

Qy 58 AATTATGCTTCAAGGGCCAGCA---TACCCCAACTTGAATGCTGTTTGGGTTGGTCC 114
Db 104 AsnTrpGlyCysIleGlyMetGlyAlaCysSerAsnSerGlnGlyIleAlaTyrTrpSer 123
Qy 115 TTAGAT-----GGTACCAGTGCCTAATCCAGGGGATACATTACATTGAATATG--- 162
Db 124 ThrAspLeuPheGlyPheTyrThrProThrAsnVal---ThrLeuGluMetThrGly 142
Qy 163 -----CCATGTGTGTTTAAATATATATCTTACAA----- 192
Db 143 TyrPheLeuProGlnThrGlySerTyrThrPheIlePheAlaThrValAspSer 162
Qy 192 ----- 192
Db 163 AlaIleLeuSerValGlyGlyAlaThrAlaPheAsnCysAlaGlnGlnProPro 182
Qy 193 ---ACATCTGTTGATTAACTGCCGATGTGTAAA----- 225
Db 183 IleThrSerThrAsnPheThrIleAspGlyIleLePheProTrpGlyGlySerLeuProPro 202
Qy 226 -----TATGCTACTTGTCAATTTTATTTCTGTGGGAAGAAATTCACAACTTTTCTACATTA 279
Db 203 AsnIleGluGlyThrValTyrMetTyrAlaGlyTyrTyrProMet----- 218
Qy 280 ACATGTACTGTGAACGACGCTTTGAATCATCATTAAGGCATTTGGTACA----- 330
Db 219 -----LysValValTyrSerAsnAlaValSerTrpGlyThrLeuProIle 233
Qy 331 ---GTTACTTTACCAATTCATTAATGTTGGTGGAAACAGGTTCATCACTGATTGGAA 387
Db 234 SerValThrLeuPro-----AspGlyThrThrValSerAspAspPheGlu 248
Qy 388 GATTCTAAATGTTTACTGCTGTGTACCAATACAGTCACATTTAATCATGTGTATAAGAT 447
Db 249 Gly-----TyrValTyrSerPheAspAsp----- 256
Qy 448 ATCTCAATTGATGTTGAGTTTGAAGAGTCAACCGTT---GATCCAAAGTGCATTTGTAT 504
Db 257 -----AspLeuSerGlnSerAsnCysThrValProAspProSerAsnTyrAla--- 272

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QY 505 GCTTCCAGAGTATGCGCAAGTCTCAATAAGGTGCACAACTCTTTTGGGCACCAACAATGT 564
Db 273 ValSerThrThrThrThrThrGluProThrThrGlyThrPheThrSerThr 292
QY 565 GAAATGGTTACACATCTGGTACAAATGGGGTTCCTCCAGTAGTAACGGGTGCTGCTATT 624
Db 293 GluMetThrThrValThrGlyThrAsnGlyValProThrAspGluThrValIleValIle 312
QY 625 GATTGCTCAATATTCATATGTTGATCACAAGAGTTAAATGATTGGAATTCACCGGTT 684
Db 313 ArgThrProThrThrAlaSerThrIleIleThrThrGluProThrPasnSerThrPhe 332
QY 685 TCATCTGAATCAATTTAGTTACACTAAACCTTGATCATCTAATGAATTCAGATTAAATAT 744
Db 333 ThrSerThrSerThrGluLeuThrThrValThrGlyThrAsnGlyValArgThrAspGlu 352
QY 745 CAAATGACCTGCTGGTTATCGTCCATTTATGATGCTTATATTTCTGCTACAGATGTT 804
Db 353 ThrIleIle-----ValIleArgThrProThrThrAlaThrThrAla 366
QY 805 AACCAATATCTTAGCATATACCAATGATTATATCTTGTGCTGGCAGTCGTCGCAAGT 864
Db 367 IleThrThrThrGluProThrPasnSerThrPheThrSerThrSerThrGluLeu----- 384
QY 865 AAACCTTTCACTTTAAGATGACTGATACCAAGATAGTATGATGCGGATCTAAGCGTATT 924
Db 385 -----ThrThrValThrGlyThrAsnGlyLeu 393
QY 925 -----GTCATTGTTGCTACAACTAGACAGTTACAGACAGTACCACTGCTGCTACT 975
Db 394 ProThrAspGluThrIleIleValIleArgThrProThrThrAlaThrThrAlaMetThr 413
QY 976 ACTTTA-----CCATTCAATCCAGTGTTCATAAACCACCAACA----- 1014
Db 414 ThrThrGlnProThrPasnAspThrPheThrSerThrSerThrGluLeuThrThrValThr 433
QY 1015 -----ATCGAAATTTTGGCAACCTATTCCCAACC 1041
Db 434 GlyThrAsnGlyLeuProThrAspGluThrIleIleValIleArgThrProThrThrAla 453
QY 1042 ACTACCATCACAACT-----TCATATGTTGGTGGTCACTACTTCC 1080
Db 454 ThrThrAlaMetThrThrThrGlnProThrPasnAspThrPheThrSerThrThrGlu 473
QY 1081 TATCTGACTAGACTGCA-----CCAAATGTTGTAACAGCTACTGTTATTGTT 1128
Db 474 LeuThrThrValThrGlyThrAsnGlyLeuProThrAspGluThr-----IleIleValIle 492
QY 1129 GATGTGCCATATCATACTACCAACA-----ACTGTTACAGTGAATGACAGCAACATC 1182
Db 493 ArgThrProThrThrAlaThrThrAlaMetThrThrThrGlnProThrPasnAspThrPhe 512
QY 1183 ACT-----ACCACCAACTCGTACCAAT-----CCAACTGATTCA 1218
Db 513 ThrSerThrSerThrGluIleThrThrValThrGlyThrAsnGlyLeuProThrAsp----- 531
QY 1219 ATTGACACAGTGGTGTA 1236
Db 532 ---GluThrIleIleVal 536
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RESULT 15
US-10-369-493-1398
; Sequence 1398, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B

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; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 1398  
; LENGTH: 1537  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-369-493-1398  
  
Alignment Scores:  
Pred. No.: 5,86e-07 Length: 1537  
Score: 177.00 Matches: 112  
Percent Similarity: 32.72% Conservative: 47  
Best Local Similarity: 23.05% Mismatches: 181  
Query Match: 7.71% Indels: 146  
DB: 15 Gaps: 25  
  
US-09-715-876-7_COPY_52_1296 (1-1245) x US-10-369-493-1398 (1-1537)  
QY 58 AATTATGCTTTCAAAGGCCCGCA--TACCRACTTTGGAATGCTGTTTGGGTGGTCC 114  
Db 104 AsnTrpGlyCysLysGlyMetGlyAlaCysSerAsnSerGlnGlyIleAlaTyTrpSer 123  
QY 115 TTAGAT-----GGTACCAGTCCCAATCCAGGGGATACATTTCACATTGAATATG- 162  
Db 124 ThrAspLeuPheGlyPheTyThrThrProThrAsnVal---ThrLeuGluMetThrGly 142  
QY 163 -----CCATGTGTGTTTAAATATATCTACTTCCAA----- 192  
Db 143 TyrPheLeuProProGlnThrGlySerTyThrPheLysPheAlaThrValAspAspSer 162  
QY 192 ----- 192  
Db 163 AlaIleLeuSerValGlyGlyAlaThrAlaPheAsnCysCysAlaGlnGlnProPro 182  
QY 193 ---ACATCTGTGATTTAACTGCGCATGGTGTAA----- 225  
Db 183 IleThrSerThrAsnPheThrIleAspGlyIleLysProTrpGlyGlySerLeuProPro 202  
QY 226 -----TATGCTACTGTCATTTTATCTGCTGGAAGAAATTCACAACTTTTCTACATTA 279  
Db 203 AsnIleGluGlyThrValTyMetTyAlaGlyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 218  
QY 280 ACATGTACTGTGAACGCGCTTTCGAAATCATCCATTAAGGCATTTGGTACA----- 330  
Db 219 -----LysValValTySerAsnAlaValSerTrpGlyThrLeuProIle 233  
QY 331 ---GTTACTTTTACCAATTTGCATTCATTTGTTGGTGGAAACAGGTTCATCACTGATTGGAA 387  
Db 234 SerValThrLeuPro-----AspGlyThrThrValSerAspAspPheGlu 248  
QY 388 GATTCTAAATGTTTACTGCTGGTACCAATACATACAGTCACATTATATGATGGTGATTAAGAT 447  
Db 249 Gly-----TyrValTySerPheAspAsp----- 256  
QY 448 ATCTCAATTCATGTTGAGTTTGAAGTCAACCGTT---GATCCAAGTGCATATTTGTAT 504  
Db 257 -----AspLeuSerGlnSerAsnCysThrValProAspProSerAsnTyAla---- 272  
QY 505 GCTTCCAGAGTTATGCGCAAGTCTCAATAAGGTGCACAACTCTTTTGGGCACCAACAATGT 564  
Db 273 ValSerThrThrThrThrThrGluProThrThrGlyThrPheThrSerThrSerThr 292  
QY 565 GAAATGGTTACACATCTGGTACAAATGGGGTTCCTCCAGTAGTAACGGGTGCTGCTATT 624  
Db 293 GluMetThrThrValThrGlyThrAsnGlyValProThrAspGluThrValIleValIle 312  
QY 625 GATTGCTCAATATTCATATGTTGATCACAAGAGTTAAATGATTGGAATTCACCGGTT 684  
Db 313 ArgThrProThrThrAlaSerThrIleIleThrThrGluProThrPasnSerThrPhe 332
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Qy 685 TCATCTGAATCAATTAGTTACACTAAACTTGTACATCTAATGAATTCAGATTAAATAT 744
Db   ::||| ||| ||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 333 ThrSerThrSerThrGluLeuThrValThrGlyThrAsnGlyValArgThrAspGlu 352
Db   ::||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 745 CAAATGTACTGCTGCTTATCGTCCATTTATTGATGCTTATATTTCTGCTACAGATTT 804
Db   ::||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 353 ThrIleIle-----ValIleArgThrProThrAlaThrThrAla 366
Db   ::||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 805 AACCAATATCTTTAGCATATACCAATGATTATATGCTGTGCGAGTCTGCTCAAGT 864
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 367 IleThrThrThrGluProIlePheSerThrSerThrSerThrGluLeu----- 384
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 865 AAACCTTTCACCTTAAAGATGCTGATACCAAGATAGTATGCGGATCTAACGGTATT 924
Db   ::||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 385 -----ThrThrValThrGlyThrAsnGlyLeu 393
Db   ::||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 925 -----GTCAATGTTGTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCAC 975
Db   ::||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 394 ProThrAspGluThrIleIleValIleArgThrProThrAlaThrThrAlaMetThr 413
Db   ::||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 976 ACTTTA---CCATTCATCCAGTGTGATAAACCAAAACA----- 1014
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 414 ThrThrGlnProThrAsnAspThrPheThrSerThrSerThrGluLeuThrValThr 433
Db   ||| ||| ::||| ::||| ::||| ::||| ::||| ::|||
Qy 1015 -----ATCGAAATTTTGCAACCTATTCCAAAC 1041
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 434 GlyThrAsnGlyLeuProThrAspGluThrIleIleValIleArgThrProThrAla 453
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 1042 ACTACCATCAAACT-----TCATATGTTGGTGTGACTACTTCC 1080
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 454 ThrThrAlaMetThrThrGlnProThrAsnAspThrPheThrSerThrSerThrGlu 473
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 1081 TATCTGACTAAGACTGCA-----CCAATTGGTGAACAGCTACTGTTATGTT 1128
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 474 LeuThrThrValThrGlyThrAsnGlyLeuProThrAspGluThr---IleIleValIle 492
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 1129 GATGTGCATATCATCTACACACA-----ACTGTTACCAAGTGAATGGACAGGAACAATC 1182
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 493 ArgThrProThrAlaThrThrAlaMetThrThrGlnProThrAsnAspThrPhe 512
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 1183 ACT-----ACCACCAACTGTCGTACCAAT-----CCAAGTGAATCA 1218
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 513 ThrSerThrSerThrGluIleThrValThrGlyThrAsnGlyLeuProThrAsp--- 531
Db   ||| ||| ||| ||| ::||| ::||| ::||| ::||| ::|||
Qy 1219 ATTGACACAGTGGTGTA 1236
Db   ::||| ::||| ::||| ::||| ::|||
Qy 532 ---GluThrIleIleVal 536
Db   ::||| ::||| ::||| ::||| ::|||
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Search completed: September 8, 2005, 18:17:05

Job time : 237 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 8, 2005, 17:29:26 ; Search time 43.5 Seconds
(without alignments)
4273.015 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296

Perfect score: 2297

Sequence: 1 aagacaatcactggtgtttt.....cagtggtggtacaattcca 1245

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/uspto_spool_p/US09715876/runat_08092005_172228_18516/app_query.fasta_1.1415
-DB=Issued Patents AA -QFWT=Eastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=blotsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09715876@cgn_1_1_46@runat_08092005_172228_18516 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pcp:*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pcp:*
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- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pcp:*
- 5: /cgn2_6/ptodata/1/iaa/PCUTS.COMB.pcp:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pcp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2170	94.5	1191	4	US-09-248-796A-16243
2	1899	82.7	780	4	US-09-248-796A-16702
3	1599	69.6	511	4	US-09-248-796A-14125
4	1545	67.3	646	4	US-09-248-796A-16701
5	1365	59.4	1060	4	US-09-248-796A-14123
6	992.5	43.2	300	4	US-09-248-796A-16245
7	984.5	42.9	812	4	US-09-248-796A-16244
8	814	35.4	229	4	US-09-248-796A-16698
9	594	25.9	232	4	US-09-248-796A-14122
10	583	25.4	154	4	US-09-248-796A-14119
11	308.5	13.4	650	3	US-08-362-525-2
12	239.5	10.7	97	4	US-09-248-796A-23586

13	192.5	8.4	501	4	US-09-248-796A-14118	Sequence 14118, A
14	189.5	8.2	386	4	US-09-248-796A-14126	Sequence 14126, A
15	177	7.7	1537	1	US-08-325-267A-2	Sequence 2, Appli
16	175.5	7.6	1837	3	US-08-928-361B-5	Sequence 5, Appli
17	175.5	7.6	1837	4	US-09-588-995A-5	Sequence 5, Appli
18	175	7.6	1721	3	US-08-700-651-5	Sequence 5, Appli
19	175	7.6	1721	3	US-08-928-361B-6	Sequence 6, Appli
20	175	7.6	1721	4	US-09-588-995A-6	Sequence 6, Appli
21	173.5	7.6	448	4	US-09-248-796A-14116	Sequence 14116, A
22	169.5	7.4	426	4	US-09-248-796A-14114	Sequence 14114, A
23	164.5	7.2	176	4	US-09-248-796A-16696	Sequence 16696, A
24	157.5	6.9	171	4	US-09-248-796A-14120	Sequence 14120, A
25	155	6.7	894	3	US-08-362-525-22	Sequence 22, Appli
26	155	6.7	894	3	US-08-971-692-15	Sequence 15, Appli
27	154	6.7	522	4	US-09-248-796A-14121	Sequence 14121, A
28	152	6.6	442	4	US-09-248-796A-26457	Sequence 26457, A
29	150.5	6.6	175	3	US-08-700-651-12	Sequence 12, Appli
30	150.5	6.6	175	3	US-08-928-361B-17	Sequence 17, Appli
31	150.5	6.6	175	4	US-09-588-995A-17	Sequence 17, Appli
32	150.5	6.6	288	4	US-09-216-393B-341	Sequence 341, App
33	150.5	6.6	288	4	US-09-216-393B-344	Sequence 344, App
34	149.5	6.5	529	4	US-09-248-796A-16703	Sequence 16703, A
35	148.5	6.5	216	3	US-08-928-361B-8	Sequence 8, Appli
36	148.5	6.5	216	4	US-09-588-995A-8	Sequence 8, Appli
37	148.5	6.5	862	1	US-08-325-267A-4	Sequence 4, Appli
38	146.5	6.4	249	3	US-08-700-651-15	Sequence 15, Appli
39	146.5	6.4	249	3	US-08-928-361B-20	Sequence 20, Appli
40	146.5	6.4	249	4	US-09-588-995A-20	Sequence 20, Appli
41	145	6.3	130	3	US-08-700-651-9	Sequence 9, Appli
42	145	6.3	130	3	US-08-928-361B-14	Sequence 14, Appli
43	145	6.3	130	4	US-09-588-995A-14	Sequence 14, Appli
44	144.5	6.3	3892	4	US-09-328-352-5503	Sequence 5503, Ap
45	144	6.3	827	4	US-09-248-796A-17307	Sequence 17307, A

ALIGNMENTS

RESULT 1

US-09-248-796A-16243
; Sequence 16243, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16243
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16243

Alignment Scores:
Pred. No.: 1.32e-194 Length: 1191
Score: 2170.00 Matches: 411
Percent Similarity: 99.52% Conservative: 2
Best Local Similarity: 99.04% Mismatches: 2
Query Match: 94.47% Indels: 0
DB: 4 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-16243 (1-1191)

QY 1 AAGCAATCACTGCTGTTTGTAGTTTATTCATTAACTGTCCCAATGCTGCTAAT 60
DB 20 LysThrIleThrGlyValPheAspSerPheAsnSerLeuThrTrpSerAsnAlaIaAsn 39

Qy	61	TATGCTTTCAAAGGCGCAGGATACCCAACTTGGAAATGCTGTTTGGGTGGTCTCTAGAT	120
Db	40	TyrAlaPheIysGlyProGlyTyrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp	59
Qy	121	GGTACCAAGTCCCAATCCAGGGGATACATTCACATTGAAATGCAATGCGTGGTTAAATAT	180
Db	60	GlyThrSerAlaAsnProGlyAspThrPheThrLeuAsnMetProCysValPheAspGlyr	79
Qy	181	ACTACTTCACAAAACATCTGTTGATTAACTGCCGATGGTGTAAATATGCTACTTGTCAA	240
Db	80	ThrThrSerGlnThrSerValAspLeuThrAlaAspGlyValIysTyrAlaThrCysGln	99
Qy	241	TTTTATTCTGGTGAAGAATTCAACATTTTCTCATTAACATGACTGTGGAACAGCGCT	300
Db	100	PheTyrSerGlyGluGluPheThrThrPheSerThrLeuThrCysThrValAsnAspAla	119
Qy	301	TTGAATCATCTCAATTAAGGCATTTGGTACAGTTACTTTTACCAATGTCATTCATGTTGT	360
Db	120	LeuIysSerSerIleIysAlaPheGlyThrValThrLeuProIleAlaPheAsnValGly	139
Qy	361	GGAAACAGGTTTCATCAACTGATTGGAAGATTTCTAAATGTTTACTGCTGGTCAACATACA	420
Db	140	GlyThrGlySerSerThrAspValGluAspSerIysCysPheThrAlaGlyThrAsnThr	159
Qy	421	GTCACTTTAATGATGGTGATAAGATATCTCAATGATGTGAGTTGAAAGTCAACC	480
Db	160	ValThrPheAsnAspGlyAspLysAspIleSerIleAspValGluPheGluLysSerThr	179
Qy	481	GTTGATCCAAGTGCATATTTGTATGCTTCCAGAGTTATGCCAGTCTCATATAGGTCACA	540
Db	180	ValAspProSerGlyTyrLeuTyrAlaSerArgValMetProSerLeuAsnLysValThr	199
Qy	541	ACTCTTTTGTGGCACCAACATGAAATGGTTTACACATCTGCTCAATGGGGTCTCC	600
Db	200	ThrLeuPheValAlaProGlnCysGluAsnGlyTyrThrSerGlyThrMetGlyPheSer	219
Qy	601	AGTAGTAACGGTGACGTTGCTATTGATTGCTCAAATATTCATATGCTATCACAAAGGA	660
Db	220	SerSerAsnGlyAspValAlaIleAspCysSerAsnIleHisIleGlyIleThrLysGly	239
Qy	661	TTAAATGATTCGAATATTCGGTTTCATCTGAATCATTTAGTTACACTAAACTGTGACA	720
Db	240	LeuAsnAspTrpAsnTyrProValSerSerGluSerPheSerTyrThrLysThrCysThr	259
Qy	721	TCTAATGGAATTCAGATTAAATATCAAAATGCTACTGCTGGTATCGTCAATTTATTGAT	780
Db	260	SerAsnGlyIleGlnIleLysTyrGlnAsnValProIleGlyTyrArgProPheIleAsp	279
Qy	781	GCTTATATTTCTGTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGATTACT	840
Db	280	AlaTyrIleSerAlaThrAspValAsnGlnTyrThrLeuAlaTyrThrAsnAspTyrThr	299
Qy	841	TGTGCTGGCAGTGTCTCCAAGTAAACCTTTCACTTTAAGATGGACTGGATACAGAAT	900
Db	300	CysAlaGlySerArgLeuGlnSerLysProPheThrLeuArgTrpThrGlyTyrLysAsn	319
Qy	901	AGTGAATGCCGATCTCAACGGTATTGTCAATCTGCTCAACTAGAACAGTTTACAGACAGT	960
Db	320	SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer	339
Qy	961	ACCACTGCTGTCACTACTCTTTTACCATTCAATCCAAAGTGTGTATAAAACCAAAACATCGAA	1020
Db	340	ThrThrAlaValThrThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu	359
Qy	1021	ATTTGCAACCTATTCCAAACCACTACCATCACTTCAATGTTGGTGTGACTACTTCC	1080
Db	360	IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer	379
Qy	1081	TATCTGCTAAGACTGCACCAATTTGGTGAACAGCTACTGTATTGTTGATGTGCCATAT	1140
Db	380	TyrLeuThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr	399
Qy	1141	CATACTACCAAACTGTTTACCAGTGAATGGACAGAACAAATCACTACCAACCAACTCGT	1200

Db 160 ValThrPheAsnAspGlySerLysLysLeuSerIleAlaValAsnPheGluLysSerThr 179
QY 481 GTTGCATCCAGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGCTCTCAATAAGGTCA 540
Db 180 ValAspGlnSerGlyTyrLeuThrThrSerArgPheMetProSerLeuAsnLysIleAla 199
QY 541 ACTCTTTTGTGGCACCACCAATGTGAAATGGTTACACATCTGGTACAAATGGGTTCTCC 600
Db 200 ThrLeuTyrValAlaProGlnCysGluAsnGlyTyrThrSerGlyThrMetGlyPheSer 219
QY 601 AGTAGTAACGGTGAGCTGTATGATGCTCAATATTCATATTCATATTCATATTCATATTC 660
Db 220 ThrSerTyrGlyAspValAlaIleAspCysSerAsnValHisIleGlyIleSerLysGly 239
QY 661 TTAATGATTCGGAATTATCCGGTTTCATCTCAATCATTTAGTACACTTAAACCTTGTACA 720
Db 240 ValAsnAspTrpAsnHisProValThrSerGluSerPheSerTyrThrLysSerCysSer 259
QY 721 TCTAATGGAATTCAGATTAAATATCAAAATGTACTGCTGTTATCGTCCATTTATTGAT 780
Db 260 SerPheGlyIleSerIleThrTyrGlnAsnValProAlaGlyTyrArgProPheIleAsp 279
QY 781 GCTTATATTTCTGCTACAGATGTTAAACCAATATATCTTAGCATATACCAATGATTACT 840
Db 280 AlaTyrIleSerProSerAspAsnAsnGlnTyrGlnLeuSerTyrLysAsnAspTyrThr 299
QY 841 TGTGCTGCGAGTCTCTCAAGTAACCTTTTCACTTTTAAGTGGAGCTGGATACAAGAT 900
Db 300 CysValAspAspTyrTrpGlnHisAlaProPheThrLeuArgTrpThrGlyTyrLysAsn 319
QY 901 AGTAGTCCGGATCTAAACGGTATTGTCTCATTTGCTCAACTAGAACAGTTTACAGACAGT 960
Db 320 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 339
QY 961 ACCACTGCTGCTACTTTTACCAATTCATCAAGTGTGATAAACCACCAACCAATCGAA 1020
Db 340 ThrThrAlaValSerThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu 359
QY 1021 ATTTGGAACTTATTCACCACTACCTACCTACCACTTATGTTGGTGGTCACTTCTCC 1080
Db 360 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 379
QY 1081 TATCTGACTTAAGACTGCACCAATGTGTAACAGCTACTGTTATTTGATGTGCTCATAT 1140
Db 380 TyrLeuThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 399
QY 1141 CATACTACCACTGTTTACAGTGAATGGACAGGACCAATCACTACCACTCACTCGT 1200
Db 400 HisThrThrThrThrValThrValThrSerGluTrpThrGlyThrThrThrThrThrArg 419
QY 1201 ACCAATCCACTGATTCATTCAGACAGTGGTGGTACAGTTCCA 1245
Db 420 ThrAsnProAsnAspSerIleAspThrValValGlnValPro 434

RESULT 3

US-09-248-796A-14125
; Sequence 14125, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14125
; LENGTH: 511
; TYPE: PRN

; ORGANISM: Candida albicans
US-09-248-796A-14125
Alignment Scores:
Pred. No.: 2,95e-141 Length: 511
Score: 1599.00 Matches: 294
Percent Similarity: 81.45% Conservative: 44
Best Local Similarity: 70.84% Mismatches: 77
Query Match: 69.61% Indels: 0
DB: 4 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-14125 (1-511)

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QY 61 TATGCTTTCAAGGGCCAGGATACCCAACTTGGATCTGTTGGGTTGGTCTTATAT 120
Db 46 TyrSerTyrArgGlyProAlaAsnProThrTyrThrAlaValIleGlyTyrSerLeuAsp 65
QY 121 GGTACCACTGCTCAATCCAGGGGATACATTACATTGAATATGCCATGTGTGTTAAATAT 180
Db 66 GlyAlaThrAlaSerAlaGlyAspThrPheThrLeuAspMetProCysValPheLysPhe 85
QY 181 ACTACTTTCACAAACATCTGTTGATTAACTGCCGATGTTTAAATATGCTTACTTGTCAA 240
Db 86 IleThrAspGlnThrSerIleAspLeuValAlaAspGlyArgThrTyrAlaThrCysAsn 105
QY 241 TTTTATTTCTGGTGAAGAAATTCACAACTTTTTCATTAATCATGATCTACTGTGACGACGCT 300
Db 106 LeuAsnSerAlaGluGluPheThrThrPheSerSerValSerCysThrValThrThr 125
QY 301 TTGAATATCATCCATTAGGCAATTTGGTACAGTTACTTTTACCATTGCAATGCAATGTTGGT 360
Db 126 MetThrAlaAspThrLysAlaIleGlyThrValThrLeuProPheSerPheSerValGly 145
QY 361 GGAACAGTTCATCAACTGATTTTGAAGATTTTAAATGTTTACTGCTGGTACCAATACA 420
Db 146 GlySerGlySerAspValAspLeuAlaAsnSerGlnCysPheThrAlaGlyIleAsnThr 165
QY 421 GTCACATTTAATGATGTGATAAAGATATCTCAATGATGATGTTGATGTTGAAAAGTCAACC 480
Db 166 ValThrPheAsnAspGlyAspThrSerIleSerAlaThrValAlaAspPheGluLysSerThr 185
QY 481 GTTGCATCCAGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGCTCTCAATAAGTCCACA 540
Db 186 ValAlaSerSerAspArgIleLeuLeuSerArgIleLeuProSerLeuSerGlnAlaVal 205
QY 541 ACTCTTTTGTGGCACCACCAATGTGAAATGTTTACACATCTGCTGATCAATGGGTTCTTCC 600
Db 206 SerLeuPheLeuProGlnGluCysAlaAsnGlyTyrThrSerGlyThrMetGlyPheSer 225
QY 601 AGTAGTAACGGTGCAGTGTGATTTGATGCTCAAAATATTCATATTCATATTCATATTCAT 660
Db 226 ThrAlaGlyThrGlyAlaThrIleAspCysSerThrValHisValGlyIleSerAsnGly 245
QY 661 TTAATGATTCGAATTTATCCGGTTTCATCTGAATCATTTAGTACACTTAACTTATGTTACA 720
Db 246 LeuAsnAspTrpAsnTyrProIleSerLeuGluSerPheSerTyrThrLysThrCysThr 265
QY 721 TCTAATGGAATTCAGATTAAATATCAAAATGCTGCTGTTATCGTCCATTTATTGAT 780
Db 266 SerThrSerValLeuValThrTyrGlnAsnValProAlaGlyTyrArgProPheValAsp 285
QY 781 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTAGCATATACCAATGATTACT 840
Db 286 AlaTyrValSerAlaThrArgValSerSerTyrAlaMetArgTyrThrAsnIleTyrAla 305
QY 841 TGTGCTGCGAGTCTCTGCAAGTAACCTTTTCACTTTTAAGTGGAGCTGGATACAAGAT 900
Db 306 CysValGlyAlaAlaSerValAspAspSerPheThrHisThrTrpLeuGlyTyrSerAsn 325

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QY 901 AGTGATCCCGGATCTAACGGTATTGTTCATTGTTGCTACAACTAGAACAGTTACAGACAGT 960
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Db 326 SerGlnAlaGlySerAsnGlyIleThrIleValValThrThrArgThrValThrAspSer 345
QY 961 ACCACTGCTGTCTACTATTACCAATTCACCAAGTGTGATTAACCAAAACAAATCGAA 1020
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Db 346 ThrThrAlaValThrThrLeuProPheAsnSerGluSerAspLysThrLysThrIleGlu 365
QY 1021 ATTTTGCACCTATTCCCAACCACTTACCATCACAACTTCATATGTTGGTGACTTCTCC 1080
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Db 366 IleLeuGlnProIleProThrThrIleThrThrSerTyrValGlyValThrThrSer 385
QY 1081 TATCTGACTAAGACTCGCACCAATTTGGTGAACAGCTACTGTTATTGTTGATGGCCATAT 1140
|||
Db 386 TyrLeuThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 405
QY 1141 CATACTACCACTGTTTACAGTGAATGACAGGAACAAATCATCTACCACCACTCGT 1200
|||
Db 406 HisThrThrThrValThrValThrSerGluTyrThrGlyThrIleThrThrThrArg 425
QY 1201 ACCAATCCAACTGATTCAATTTGACACAGTGTGTACAAAGTTCCA 1245
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Db 426 ThrAsnProThrAspSerIleAspThrValValGlnValPro 440

RESULT 4
US-09-248-796A-16701
; Sequence 16701, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16701
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16701

Alignment Scores:
Pred. No.: 3,79e-136 Length: 646
Score: 1545.00 Matches: 286
Percent Similarity: 81.53% Conservative: 54
Best Local Similarity: 68.59% Mismatches: 75
Query Match: 67.26% Indels: 2
DB: 4 Gaps: 1

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-16701 (1-646)
QY 1 AAGCAATCACTGGTGTGTTTATGATGTTTAAATTCATTAACTTGTGTCCTCAATGCTGTAAT 60
|||
Db 37 LysThrIleSerGlyValPheThrSerPheAsnSerLeuThrThrIleThrThrAsnThrGlyAsn 56
QY 61 TATGCTTTCAAGGCCGAGGATACCAACTTGGAAATGCTGTTTGGGTGTGTCCTTAGAT 120
|||
Db 57 TyrProTyrGlyGlyProGlyTyrProThrThrAlaValLeuGlyTyrSerLeuAsp 76
QY 121 GGTACCAAGTGCATCCAGGGGATACATTCATTAATGATGATGCTGTTTAAATAT 180
|||
Db 77 GlyThrLeuAlaSerProGlyAspThrPheThrLeuValMetProCysValPheLysPhe 96
QY 181 ACTACTTCACAAACATCTGTTGATTAACTCCCGATGGTGTAAATATGCTACTTGTCAA 240
|||
Db 97 IleThrThrGlnThrSerValAspLeuThrAlaAsnGlyValLysTyrAlaThrCysThr 116
QY 241 TTTTATTCTGTGAAGATTCACAACTTTTCTATCAATTAACATGTAAGTGTGGAACGAGCT 300
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Db 117 PheHisAlaGlyGluAspPheThrThrPheSerSerMetSerCysValValAsnAsnGly 136
|||
QY 301 TTGAAATCATCATTAAGGCAATTTGGTACAGTTTACTTTTACCAATTCGATTCAATGTGTGT 360
|||
Db 137 LeuSerSerAsnIleArgAlaPheGlyThrValArgLeuProIleSerPheAsnValGly 156
QY 361 GGAACAGGTTTCATCAACTGATTGGGAAGATTCTAAATGTTTACTGCTGCTGCTACCAATACA 420
|||
Db 157 GlyThrGlySerSerValAsnIleGlnAspSerLysCysPheThrAlaGlyThrAsnThr 176
QY 421 GTCACATTTAATGATGGTGCATAAAGATATCTCAATTCGATGTTTCAGTTTGAAGTCAACC 480
|||
Db 177 ValThrPheThrAspGlyAspHisLysIleSerThrThrValAsnPheProLysThrPro 196
QY 481 GTTGATCCAAAGTGCATATTTGTATGCTTCAGAGTTTATGCCAAGTCTCAATAAGGTGCACA 540
|||
Db 197 GlnSerSerSerSerLeuValTyrPheAlaArgValIleProSerLeuAspLysLeuSer 216
QY 541 ACTCTTTTGTGGCCACCAATGTGAAATGGTTACACATCTGGTACAAATGGGGTTCTCC 600
|||
Db 217 SerLeuValValAlaSerGlnCysThrAlaGlyTyrAlaSerGlyValLeuGlyPheSer 236
QY 601 AGTAGTAACGGTGACGCTGCTATTCGCTCAATATTCATATTCATATTCGTTATCACAAGGA 660
|||
Db 237 AlaThrLysAspAspValThrIleAspCysSerThrIleHisValGlyIleThrAsnGly 256
QY 661 TTAATGATTGGAATTCATCCGGTTTCATCTGAATCATTTAGTTTACATAAACTGTGACA 720
|||
Db 257 LeuAsnSerTyrAsnMetProValSerSerGluSerPheSerTyrThrLysThrCysThr 276
QY 721 TCTAATGGAATTCAGATTAATCAAAATGACCTGCTGGTGTATCGTCATTATTTGAT 780
|||
Db 277 ProAsnSerPheIleIleThrTyrGluAsnValProAlaGlyTyrArgProPheIleAsp 296
QY 781 GCTTATATT-----TCTGCTACAGATGTTAAACCAATATATCTTACCATATACCAATGAT 834
|||
Db 297 SerTyrValLysLysSerAlaThrAlaThrAsnGlyPheAsnLeuAsnTyrThrAsnIle 316
QY 835 TATACTTGTGCTGGCAGTCTCTGCAAGTAAACCTTTTCACTTTAAGATGGAGCTGGATAC 894
|||
Db 317 TyrAsnCysMetAspGlyLysLysGlyAsnAspProLeuIleTyrPheTyrThrSerTyr 336
QY 895 AAGAATAGTAGCCCGATCTAACGGTATTTGTCATTGTTGCTTACCACTAGAACAGTTTACA 954
|||
Db 337 ThrAsnSerAspAlaGlySerAsnGlyAlaAlaValValThrThrArgThrValThr 356
QY 955 GACAGTACCACTGCTGCTCACTACTTACCAATTCACCAATTCACCAATTCACCAATTCACCA 1014
|||
Db 357 AspSerThrThrAlaIleThrThrLeuProPheAspProThrValAspLysThrLysThr 376
QY 1015 ATCGAAATTTGCAACTATTCCAAACCACTTACCATCACAACTTCATATGTTGGTGTGACT 1074
|||
Db 377 IleGluValIleGluProIleProThrThrThrIleThrThrSerTyrValGlyIleSer 396
QY 1075 ACTTCTCTATCTGACTAAGACTGCACCAATTTGGTGAACACAGCTACTGTTATTTGTTGATG 1134
|||
Db 397 ThrSerLeuSerThrLysThrAlaThrIleGlyGlyThrAlaThrValValValAspVal 416
QY 1135 CCATTCATCTACTACCACTGTTTACAGTGAATGACAGGACCAATCACTACCAACCA 1194
|||
Db 417 ProTyrHisThrThrThrIleThrSerIleTyrThrGlySerThrThrThrSerSer 436
QY 1195 ACTCGTACCAATCAACTGATTCAATTCACCAAGTGTGTTGTTGTTGTTGTTGTTGTTGTT 1245
|||
Db 437 ThrTyrThrAsnProThrAspSerIleAspThrValValGlnValPro 453

RESULT 5
US-09-248-796A-14123
; Sequence 14123, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
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;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A

;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 14123
;; LENGTH: 1060
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-09-248-796A-14123

Alignment Scores:
Pred. No.: 3,54e-119 Length: 1060
Score: 1365.00 Matches: 255
Percent Similarity: 92.05% Conservative: 23
Best Local Similarity: 84.44% Mismatches: 24
Query Match: 59.43% Indels: 0
DB: 4 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-14123 (1-1060)

QY	340	CCAAATGCAATTCATGTTGGGACAGGTTTCATCACTGATTGGGAAGATTCTAAATGT	399
DB	9	ProValValLysAsnValGlyThrGlySerValAspLeuGluaspSerLysCys	28
QY	400	TTTACTGCTGTACCAATACAGTACATTTAATGATGTTGATAAGATATCTCAATTGAT	459
DB	29	PheThrAlaGlyThrAsnThrValThrPheAsnAspGlyGlyLysLysLysSerIleAsn	48
QY	460	GTTGATTTGAAAAGTCAACCGTTGATCCAAAGTCATATTTGTTATGCTTCAGAGTTATG	519
DB	49	ValAspPheGluArgSerAsnValAspProLysGlyTyrLeuThrAspSerArgValIle	68
QY	520	CCAACTCTCAATAGGTACAACTCTTTTGGCCACCACTGAAATGGAATGGTTTACACA	579
DB	69	ProSerLeuAsnLysValSerThrLeuPheValAlaProGlnCysAlaAsnGlyTyrThr	88
QY	580	TCTGTGTACAAATGGGTTCTCCAGTAGTAACCGTTGACGTTGCTATTGATTGCTCAAAAT	639
DB	89	SerGlyThrMetGlyPheAlaAsnThrTyrGlyAspValGlnIleAspCysSerAsnIle	108
QY	640	CATATTTGTTATCACAAGGATTAATGATGGAAATATCCGGTTTCACTGAATCATTT	699
DB	109	HisValGlyIleThrLysGlyLeuAsnAspTrpAsnTyrProValSerSerGluSerPhe	128
QY	700	AGTTACACTAAACTGTTGATCTAATGGAATTCAGATTAATATCAAAATGTACCTGCT	759
DB	129	SerTyrThrLysThrCysSerSerAsnGlyIlePheIleThrTyrLysAsnValProAla	148
QY	760	GTTATCTGTCATTTATTGATGCTTATATTTCTGCTACAGATGTTTAAACCAATATCTTTA	819
DB	149	GlyTyrArgProPheValAspAlaTyrIleSerAlaThrAspValAsnSerTyrThrLeu	168
QY	820	GCATATACCAATGATTATCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	879
DB	169	SerTyrAlaAsnGluTyrThrCysAlaGlyGlyTyrTrpGlnArgAlaProPheThrLeu	188
QY	880	AGATGCTGGATACAGAAATGATGATCCGGATCTAAGGTTATGTTGTTGTTGCTTACA	939
DB	189	ArgTrpThrGlyTyrArgAsnSerAspAlaGlySerAsnGlyIleValIleValAlaThr	208
QY	940	ACTAGAACATTTACAGACAGTACCACTGCTGTCCTACTTTTACCATTCAATCCAAAGTGT	999
DB	209	ThrArgThrValThrAspSerThrThrAlaValThrLeuProPheAspProAsnArg	228
QY	1000	GATAAAACCAAAACCAATCGAAATTTTGGCACTATTTCACCACTACCATCACTTCA	1059
DB	229	AspLysThrLysThrIleGluIleLeuLysProIleProThrThrThrIleThrThrSer	248

QY	1060	TATGTTGGTGTGACTACTTCTCTATCTGACTTAAGACTGCACCAATTTGGTGAACAGCTACT	1119
DB	249	TyrValGlyValThrThrSerTyrLeuThrLysThrAlaProIleGlyGluThrAlaThr	268
QY	1120	GTTATTTGTCATGTGTCATATCATCTACCACTGTTTACCAGTGAATCGACAGGAACA	1179
DB	269	ValIleValAspIleProTyrHisThrThrThrValThrSerLysThrThrGlyThr	288
QY	1180	ATCACTACCAACCAACTCGTACCAATCCAACTGATTCAATTCACACAGTGGTGTACAA	1239
DB	289	IleThrSerThrThrHisThrAsnProThrAspSerIleAspThrValIleValGln	308
QY	1240	GTTTCCA 1245	
DB	309	ValPro 310	

RESULT 6
US-09-248-796A-16245
; Sequence 16245, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16245
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (289)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk
US-09-248-796A-16245

Alignment Scores:
Pred. No.: 1,62e-84 Length: 300
Score: 992.50 Matches: 189
Percent Similarity: 84.17% Conservative: 13
Best Local Similarity: 78.75% Mismatches: 37
Query Match: 43.21% Indels: 1
DB: 4 Gaps: 1

QY	526	CTCAATTAAGTGCACAACTCTTTTGTGGCCACCACTGTAATGTAATGTTTACACATCTGTT	585
DB	8	LeuThrLysLeuGlnSerLeuMetTrpGlnProGlnCysAlaAsnGlyTyrThrSerGly	27
QY	586	ACAATGGGTTCTCCAGTAGTAACCGTGACGTTGCTATTGCTCAAAATATTCAATTT	645
DB	28	AlaMetGlyPheIleValLeuThrGlyAspThrThrIleAspCysSerAsnValHisVal	47
QY	646	GGTATCAAAAAGGATTAAATGATTGGAATTTATCCGGTTTTCATCTGAATCAATTTAGTTAC	705
DB	48	GlyIleThrLysGlyLeuAsnAspTrpAsnPheProValSerSerAspSerLeuSerTyr	67
QY	706	ACTAAAATCTGTACATCTAATGGAATTCAGATTAATATCAAAATGTAATGCTGCTGTTAT	765
DB	68	AsnLysThrCysSerSerThrGlyIleSerIleThrTyrGluMetPheProAlaGlyTyr	87
QY	766	CGTCCATTTATTGATGCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCATAT	825
DB	88	ArgProPhePheAspValTyrThrLeuValSerAspGlnAsnArg---GlnLeuLysTyr	106

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QY 826 ACCAATGATTATCTTGTGCTGGCAGTCGTCGCAAGTAACCTTTCACTTTAAGATGG 885
DB 107 ThrAsnAspTyrAlaCysValGlySerSerLeuGlnSerLysProPheAsnLeuArgLeu 126
QY 886 ACTGGATACAAGAAATAGTATGCGGATCTAAGTATGTCATTTGCTCACTACACTAGA 945
DB 127 ArgGlyTyrAsnAsnSerGluAlaAsnSerAsnGlyPheValIleValAlaThrThrArg 146
QY 946 ACAGTTACAGACAGTACACTGCTGCTCACTACTTACCACTTCACTCAAGTGTGTATAA 1005
DB 147 ThrValThrAspSerThrThrAlaValThrLeuProPheAsnProSerIleAspLys 166
QY 1006 ACCAAAAACAATCGAAATTTTGCACACCTATTCCCACTACCACTCACTCACTTATGTT 1065
DB 167 ThrLysThrIleGluIleLeuGlnProIleProThrThrThrThrThrThrThrThrVal 186
QY 1066 GGTGTGACTACTTCTCTACTGACTAAGACTGACCACTGACCAATGCGTGAACAGACTACTGTTAT 1125
DB 187 GlyValSerThrSerTyrLysThrLysThrAlaProIleGlyGluThrAlaThrValIle 206
QY 1126 GTTGATGTCATATCATCTACCACTGACCACTGTTACCACTGCAATGGACAGCAACATCACT 1185
DB 207 ValAspValProTyrHisThrThrThrThrValThrSerGluThrThrGlyThrIleThr 226
QY 1186 ACCACCAACAACCTGCTACCAATCCAACTGATTCATTTGACACAGTGGTGGTACAGTTCCA 1245
DB 227 ThrThrThrThrArgThrAsnProThrAspSerIleAspThrValValGlnValPro 246

RESULT 7
US-09-248-796A-16244
; Sequence 16244, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16244
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16244

Alignment Scores:
Pred. No.: 1,45e-83 Length: 812
Score: 984.50 Matches: 194
Percent Similarity: 63.46% Conservative: 70
Best Local Similarity: 46.63% Mismatches: 151
Query Match: 42.86% Indels: 1
DB: 4 Gaps: 1

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-16244 (1-812)
QY 1 AAGACAATCACTGCTGTTTTGTAGATGTTTAAATTCATTAACCTGGTCCAAATGCTGTAAT 60
DB 29 LysGluValThrGlyValPheAsnGlnPheAsnSerLeuIleTyrSerTyrThrTyrArg 48
QY 61 TATGCTTTCAAGCGCCAGGATACCCAACTTGGAATGCTGTTTGGGTGGTCTCTAGAT 120
DB 49 AlaArgTyrGluGluIleSerThrLeuThrAlaLysAlaGlnLeuGluThrAlaLeuAsp 68
QY 121 GGTACCAAGTGCATTCAGGGGATACATTCATTTGAATATGCACTGCTGTTTAAATAT 180
DB 69 GlyThrIleAlaSerProGlyAspThrPheThrLeuValMetProCysValTyrLysPhe 88
QY 181 ACTACTTCACAAACATCTGTTGATTTTAACTGCCGATGGTGTAAATATATGCTACTTGTCAA 240
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DB 89 MetThrTyrGluThrSerValGlnLeuThrAlaAsnSerIleAlaTyrAlaThrCysAsp 108
QY 241 TTTTATCTCTGGTGAAGAATTCACACTTTTCTACATTAACTACTGCTGTAACGACGCT 300
DB 109 PheAspAlaGlyGluAspThrLysSerPheSerSerLeuLysCysThrValThrAspGlu 128
QY 301 TTGAATCATCATCAATTAAGGCATTTGGTACAGTTACTTTTACCAATTTGCAATTTCAATTTGGT 360
DB 129 LeuThrGluAspThrSerValPheGlySerValIleLeuProIleAlaPheAsnValGly 148
QY 361 GGAACAGGTTCATCAACTGATTTTGAAGATTCCTAAATGTTTACTCTGCTGGTACCAATACA 420
DB 149 GlySerGlySerLysSerThrIleThrAspSerLysCysPheSerSerGlyTyrAsnThr 168
QY 421 GTCACATTTAAATGATGCTGATAAAGATATCTCAATTTGATTTGAGTTTCAAAAGTCAACC 480
DB 169 ValThrPhePheAspGlyAsnAsnGlnLeuSerThrThrAlaAsnPheLeuProArgArg 188
QY 481 GTTGATCCCAAGTGCATATTTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATTAAGGTCACA 540
DB 189 GluLeuAlaPheGlyLeuValSerGlnArgLeuSerMetSerSerLeuAspThrMetThr 208
QY 541 ACTCTTTTGTGGCCACCAATGCTGAAATGGTTACACATCTGCTGTAACATGGGTTCTCC 600
DB 209 AsnPheValMetSerThrProCysPheMetGlyTyrGlnLeuGlyLysLeuGlyPheThr 228
QY 601 AGTAGTAACGGTGCACCTGCTTATGCTCAATATTCATATTCATATTCATATTCATATTCAT 660
DB 229 SerAsnAspAspAspPheGluIleAspCysSerSerIleHisValGlyIleThrAsnGlu 248
QY 661 TTAATATGATTTGAATTTATCCGGTTTCATCTGAATCATTTAGTTTACATAAACTTGTACA 720
DB 249 IleAsnAspTyrSerMetProValSerSerValProPheAspHisThrIleArgCysThr 268
QY 721 TCTAATGGAATTCAGATTAATATCAAAATGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 269 SerArgAlaLeuTyrIleGluPheLysThrIleProAlaGlyTyrArgProPheValAsp 288
QY 781 GCTTATATTTCTGCTACAGATGTTAACCAATATATCTTTAGCATATATACCAATGATTATACT 840
DB 289 AlaIleValGlnIleProThrThrGluProPhePheValLysTyrThrAsnGluPheAla 308
QY 841 TGTGCTGGCAGTGTCTGCAAAAGTAAACCTTTTCACTTTTAAAGATGGACT---GGATACAAG 897
DB 309 CysValAsnGlyIleTyrThrSerIleProPheThrSerPhePheSerGlnProIleLeu 328
QY 898 AATAGTGTATGCCGATCTAACCGTATTGTCATTTGCTTACACTAGACAGTACAGTACAGAC 957
DB 329 TyrAspGluAlaLeuAlaIleGlyAlaAspLeuValArgThrThrSerThrValIleGly 348
QY 958 AGTACCACCTGCTGCTCACTACTTTTACCATTCAATCCCAAGTGTGATATAAAACCAAAATC 1017
DB 349 SerIleThrArgThrThrThrLeuProPheIleSerArgLeuGlnLysThrLysThrIle 368
QY 1018 GAAATTTGCAACTTATCCAACTACATACCACTTCACTTCAATATGCTGCTGCTGCTGCTGCT 1077
DB 369 LeuValLeuGluProIleProThrThrThrValThrThrSerHisGlyPheAspThr 388
QY 1078 TCTATCTGACTTAAGACTGCACCAATTTGTTGAACAGCTACTGCTTATTTGTTGATGTGCCA 1137
DB 389 TrpTyrTyrThrLysLysAlaThrIleGlyAspThrAlaThrValPheIleAspValPro 408
QY 1138 TATCATACTACCACTGTTTACAGTGAATGACAGGAACTACTACTACCACCACT 1197
DB 409 GlnHisThrAlaThrThrLeuThrThrTyrTyrTyrGlnGluSerSerThrAlaThrThrThr 428
QY 1198 CGTACCAATCCAACTGATTCATTAATTTGACAGTGGTGGTCAAGTTCCA 1245
DB 429 TyrPheAspAspIleAspLeuValAspThrValIleValIleValIlePro 444

RESULT 8
US-09-248-796A-16698
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/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 14119
/ LENGTH: 154
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-09-248-796A-14119

Alignment Scores:
Pred. No.: 2,87e-46 Length: 154
Score: 583.00 Matches: 111
Percent Similarity: 83.44% Conservative: 15
Best Local Similarity: 73.51% Mismatches: 25
Query Match: 25.38% Indels: 0
DB: 4 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-14119 (1-154)
Qy 679 CCGGTTTCATCATGATCAATTTAGTACACATAAACTTGTACATCAATGAATTCAGATT 738
Db 4 ProglySerSerGluSerPheSerTyThrLysThrCysThrSerThrSerIleThrVal 23
Qy 739 AATATCAAAATGACTGCTGCTGTTATGTCCTCATTTATGATGCTTATATTTCTGTACA 798
Db 24 GluPheGlnAsnValProAlaGlyTyArgProPheValAspAlaTyIleSerAlaGlu 43
Qy 799 GATGTTAAACAATATCTTTAGCATATACCAATGATTATCTTGTGTCGAGTCGTCG 858
Db 44 AsnIleAspLysTyThrLeuThrTyAlaAsnGluTyThrCysGluAsnGlyAsnThr 63
Qy 859 CAAAGTAAACCTTTCACTTTAAGATGGACTGGATACAGAATAGTATGCGGATCTAAC 918
Db 64 ValValAspProPheThrLeuThrTyrGlyTyIleAsnSerGluAlaAspSerAsp 83
Qy 919 GGTATTTGTCATTTGTCACACTAGAACAGTTACACAGTACAGACAGTACCTGTCGACTACT 978
Db 84 GlyAspValIleValValThrArgThrValThrAspSerThrThrAlaValThrThr 103
Qy 979 TTACCATTCATCAACAGTGTGTGATAAAACCAAAACATCGAAATTTTGCAACCTATTCCA 1038
Db 104 LeuProPheAsnProSerValAspLysThrGluThrIleGluIleGluLeuGlnProIlePro 123
Qy 1039 ACCACTACCATCAACATTCATATGTTGGTGTGACTACTTCCTATCTGACTAAGACGTGCA 1098
Db 124 ThrThrIleThrThrSerTyIleGlyIleSerThrSerTyGluThrLeuThrGly 143
Qy 1099 CCAATTCGTGAAACAGTACTGTTATTGTTGAT 1131
Db 144 ThrIleGlyGlyThrAlaThrValIleValAsp 154

RESULT 11
US-08-362-525-2
/ Sequence 2, Application US/08362525
/ Patent No. 6027910
/ GENERAL INFORMATION:
/ APPLICANT: KLIS, FRANCISCUS M.
/ APPLICANT: SCHREUDER, MAARTEN P.
/ APPLICANT: TOSCHKA, HOLSER Y.
/ APPLICANT: VERRIPS, CORNELIS T.
/ TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
/ CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
/ PROTEIN
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: CUSHMAN DARB & CUSHMAN, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
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/ STATE: D. C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/362,525
/ FILING DATE: 04-JAN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 92202080.5
/ FILING DATE: 08-JUL-1992
/ PRIOR APPLICATION NUMBER: EP 92203899.7
/ FILING DATE: 14-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP93/01763
/ FILING DATE: 07-JUL-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KOKULIS, PAUL N.
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: 213289/T7020(V)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 861-3000
/ TELEFAX: (202) 822-0944
/ TELEX: 6714627 CUSH
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 650 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-362-525-2

Alignment Scores:
Pred. No.: 3e-20 Length: 650
Score: 308.50 Matches: 116
Percent Similarity: 43.33% Conservative: 79
Best Local Similarity: 25.78% Mismatches: 190
Query Match: 13.43% Indels: 65
DB: 3 Gaps: 20

US-09-715-876-7_COPY_52_1296 (1-1245) x US-08-362-525-2 (1-650)
Qy 25 AGTTTAAATTCATTACTTGGTCCAAAT-----CCTGCTAATTATGCT 66
Db 21 AsnIleAsnAspIleThrPheSerAsnLeuGluIleThrProLeuThrAlaAsn----- 38
Qy 67 TTCAAAGGCGCAGGATACCAACTTGAATGCTGTTTGGTGGTCTTTA---GATGGT 123
Db 39 ---LysGlnProAsp---GlnGlyThrAlaThrPheAspPheSerIleAlaAspAla 56
Qy 124 ACCAGTGCCAATCCAGGGGATACATTCACATTGAATATGCCATGTGTGTTTAA----- 177
Db 57 SerSerIleArgGluGlyAspGluPheThrLeuSerMetProHisValTyArgIleLys 76
Qy 178 ---TATACTACTTCACAAACATCTGTGATTTAACTGCCGATGGTGTAAATATGCTACT 234
Db 77 LeuLeuAsnSerSerGlnThrAlaThrIleSerLeuAlaAspGlyThrGluAlaPheLys 96
Qy 235 TGTCAATTTTATTCTGCTGAA-----GAATTCACAACTTTTCTACATTA 279
Db 97 Cys---TyrValSerGlnGlnAlaAlaTyLeuTyThrGluAsnThrThrPhe----- 112
Qy 280 ACATGTACTGTGAACGACGCTTTGAAATCATCATTAAGCATTTGGTACAGTACTTTTA 339
Db 113 ThrCysThrAlaGlnAsnAspLeuSerSerTyAsnThrIleAspGlySerIleThrPhe 132
Qy 340 CCAATTCGATTCATGTTGGTGAACAGGTTTCATCACTGATTCATGAAGATTCCTAAATGT 399
```

Db 133 SerLeuAsnPheSerAspGlySerSerTyrGluTyrGluLeuGluAsnAlaLysPhe 152
Qy 400 TTTACTGCTGCTACCAATACAGTCACATTTAATGATGCTGATGAAGATATCTCAATTGAT 459
Db 153 PheLysSerGlyProMetLeuValLysLeuGlyAsnGlnMetSerAspVal-----169
Qy 460 GTTGAGTTTGAAGAAGTCAACGGTTGATCCAAAGTGCATAT-----TTGATGCTTCC 510
Db 170 ValAsnPhe-----AspProAlaAlaPheThrGluAsnValPheHisSer 184
Qy 511 AGAGTTATGCCAGTCTCAATAAGGTCAACTCTTTTGGGCACCAATGTGAAT 570
Db 185 GlyArgSerThrGlyTyrGlySerPheGluSerTyrHisLeuGlyMetTyrCysProAsn 204
Qy 571 GGTTCACATCTGCT-----ACAATGGGGTCTCCAGTGTAGTAAACGGTGGCTGCT 621
Db 205 GlyTyrPheLeuGlyGlyThrGluLysIleAspTyrAspSerSerAsnAsnValAsp 224
Qy 622 ATTGATTGCTCAATATTATATATGTTATGTTATCAAAAGGATTAAATGATTGGAATATCCG 681
Db 225 LeuAspCysSerSerValGlnValTyrSerSerAsnAspPheAsnAspTyrTyrPhePro 244
Qy 682 GTTTCATCTGAATCATTTAGTTACACTAAACTGTGTACATCTAATGGAATTCAGATTAA 741
Db 245 GlnSerTyrAsnAspThrAsnAlaAspValThrCysPheGlySerAsnLeuTyrPheThr 264
Qy 742 TAT---CAAAATGACCTGCTGTTATCGTTCATTTATGATGCTATATTTCT---GCT 795
Db 265 LeuAspGluLysLeuTyrAspGlyGluMetLeuTyrValAsnAlaLeuGlnSerLeuPro 284
Qy 796 ACAGATGTTAAACCAATATATTAGCATATACCAATGATTATCTTGT-----843
Db 285 AlaAsnValAsnThrIleAspHisAlaLeuGluPheGlnTyrThrCysLeuAspThrIle 304
Qy 844 GCTGTCAGTCTGCTGCAAGTAACCTTTTCACTTTTAAAG-----TGGACTGGA 891
Db 305 AlaAsnThrThrTyrAlaThrGlnPheSerThrThrArgGluPheIleValTyrGlnGly 324
Qy 892 TACAAGATAGTAGTGCCTGATCTAACCGTATTGTCATTTGCTACAACTAGACAGTT 951
Db 325 ArgAsnLeuGlyThrAlaSerAlaLysSerSerPheIleSerThrThrThrAspLeu 344
Qy 952 ACAGAC-----AGTACCAGTCTGCTGCTACCTATTACCATTTCAATCA 993
Db 345 ThrSerIleAsnThrSerAlaTyrSerThrGlySerIleSerThrVal-----360
Qy 994 AGTGTGTATAAACCAACCAATCGAAATTTGCAACCTATTCCAACTACCATCA 1053
Db 361 GluThrGlyAsnArgThrThrSerGluValIleSerHisValValThrThrSerThrLys 380
Qy 1054 ACTTCATATGTTGGTGACTACTCTCCTATCTGACTAGACTGACCAATGGTGAACA 1113
Db 381 LeuSerProThrAlaThrThrSerLeuThrIleAlaGlnThrSerIleTyrSerThrAsp 400
Qy 1114 GCTACTGTTATTTGTTGATGTCATATACATACACAC-----1152
Db 401 SerAsnIleThrValGlyThrAspIleHisThrThrSerGluValIleSerAspValGlu 420
Qy 1153 ACTGTTACAGTGAATGACAGCAACAAATCACTACCACTACCACTACCACTACCACTACCA 1209
Db 421 ThrIleSerArgGluThrAlaSerThrValAlaAlaProThrSerThrThrGlyTyr 440
Qy 1210 ACTGATTCATTTGACAGTGTGTGTACAA 1239
Db 441 ThrGlyAlaMetAsnThrTyrIleProGln 450

RESULT 12
US-09-248-796A-23586
; Sequence 23586, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23586
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23586
Alignment Scores: 3.64e-14 Length: 97
Pred. No.: 239.50 Matches: 54
Score: 67.39% Conservative: 8
Best Local Similarity: 58.70% Mismatches: 27
Query Match: 10.68% Indels: 3
DB: 4 Gaps: 1
US-09-715-876-7_COPY_52_1296 (1-1245) x US-09-248-796A-23586 (1-97)
Qy 494 GCACCTTGATCA-----ACGTTGACTTTTCAAACTCAACATCAATGTGATATCT 444
Db 6 AlaAlaGlySerGlyHisAspThrGlyAspAlaSerLysSerThrValValGluIlePhe 25
Qy 443 TTATCACCATCATTAATGATGCTGTTATGGTACCAGCAGTAAACATTTAGATCTTCC 384
Db 26 ValSerProSerMetLysValThrValPheProAlaValLysHisLeuGluSerAla 45
Qy 383 AAATCAGTTGATGACCTGTTCCACCAACATTCGAATGCAATGTAAGTAAGTAACTGTACCA 324
Db 46 LysSerThrGluGluProValProThrLeuAsnValMetGlyAsnLeuThrValPro 65
Qy 323 AATGCCCTTAATGGATGATTTCAAGCGCTGTTCCAGTACATGTTAATGTAGAAAAAGTT 264
Db 66 GluThrLeuAlaTyrAspThrGluThrLeuPheThrValHisAspLysGluGluAsnVal 85
Qy 263 GTGAATTTCTCACCAGAAATAAATTGACAAGTAGCA 228
Db 86 ValAsnSerSerProAlaLeuLysSerGlnValAla 97

RESULT 13
US-09-248-796A-14118
; Sequence 14118, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14118
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14118
Alignment Scores: 1.98e-09 Length: 501
Pred. No.: 192.50 Matches: 108
Score: 36.48% Conservative: 58
Best Local Similarity: 23.74% Mismatches: 170
Query Match: 8.38% Indels: 119

71 ArgGluProProAsnProThrValThrThrThrGluTyrTrpSerGlnSerTyrAlaThr 90
322 TTTGGTACAGTACTTTTACCAATTCGATTCAATGTTGGTGGTGAACAGGTTCA----- 372
91 ThrThrThrValThrAlaPro-----ProGlyGlyThrAspSerValIlelle 106
373 -----TCAACTGATTGGGAAGATTCTAAATGTTTACTGCT 408
107 ArgGluProProAsnProThrValThrThrGluTyrTrpSerGlnSerPhe---Ala 125
409 GGTACCAATCAGTCACATTAATGATGGTGAATAAGATATCTCAATGATGTTGAGTTT 468
126 ThrThrThrValThrAlaProProGlyGlyThrAspSerValIlelleArgGluPro 145
469 GAAAGTCAACCGTTGATCCAGTGCATATTGTTGATGCTCCAGAGTTATGCCAAGTCTC 528
146 ProAsnProThrValThrThrThrGluTyrTrpSerGlnSerTyrAla----- 161
529 AATAAGGTCACAACTCTTTTGTGGCCACCAATGTCGAAATGTTACACATCTGTGTA 588
162 -----ThrThrThrValThrAlaProPro-----GlyGlyThrAspSerVal 176
589 ATGGGGTTCACAGTAGTAAACGGTGGTGTGTTGATGCTCAATATATTCATATGGT 648
177 IlelleArgGluProProAsnProThrValThr----- 188
649 ATCACAAGGATTAATGATGTAATATCCGGTTTCATCTGAATCATTTAGTTACACT 708
189 -----ThrGluTyrTrp-----SerGlnSerTyrAlaThr 199
709 AAAACTTGTATCATTAATGATGTAATATCCGGTTTCATCTGAATCATTTAGTTACACT 768
200 ThrThrValThrAla-----ProProGlyGly----- 208
769 CCATTTATGATGTTATTTCTGCTACAGATGTTAACAAATATCTTAGCATATACC 828
209 -----ThrAlaThrValIlelleArgGluProProAsnTyrThr 221
829 AATGATTATACTTGTGTCGCGATCTGCAAGATTAACCTTTCACCTTAAAGATGACT 888
222 -----ValThrThrThrGluTyrTrpSerGlnSerTyrAlaThrThrThrIleThr 239
889 GGATACAAGATAGTATGTCGCGATCTAACGGTATTGTCATT----- 930
240 Ala-----ProProGlyGlyThrAspThrValIlelleArgGluProProAsnTyr 256
931 ---GTTGTACAACTAGAACAGTTCACAGACAGTACCACTGCTGCTACTTACCATTC 987
257 ThrValThrThrThrGluTyrTrpSerGlnSerTyrThrThrThrValThrGly 276
988 AATCAAGTGTGATAAACCAACAAATTCGAATTTGCAACCTATTCGACCACTACC 1047
277 ProProGly-----GlyThrAspThrValIlelleArgGluPro---ProAsnTyrThr 293
1048 ATCACAACT-----TCATATGTTGGTGTGACTTCTCTATCTGACT 1089
294 ValThrThrThrGluTyrTrpSerGlnSerTyrAlaThrThr-----Thr 309
1090 AAGACTGCACCAATTTGGTGAACAGTACTGTTATGTTGATGTCGCATATCATACTACC 1149
310 ValThrGlyProProGlyGlyThrAspThrValIlelleArgGluProProAsnTyrThr 329
1150 ACACTGTTACAGTGAATGACAGGAAATCATCTACCAACCACTGCTGACCAATCCA 1209
330 ValThrThrThrGluTyrTrpSerGlnSerTyrAlaThrThrThrThrValThrGlyPro 349
1210 ACTGATTCATTTGACACAGTGTGTACAAAGTTCCA 1245
350 ProGlyGlyThrAspThrValIlelleArgGluPro 361

RESULT 15
US-08-325-267A-2
; Sequence 2, Application US/08325267A

Patent No. 5585271
GENERAL INFORMATION:
APPLICANT: WATARI, JUNJI
APPLICANT: TAKATA, YOSHIHIRO
APPLICANT: OGAWA, MASAHIRO
APPLICANT: PENTTILA, MERJA
APPLICANT: ONNELA, MAIJA-LEENA
APPLICANT: KERANEN, SIRKKA
TITLE OF INVENTION: YEAST AGGLUTINATION GENES AND YEAST
TITLE OF INVENTION: CONTAINING THEM
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,267A
FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP PCT/JP94/00290
FILING DATE: 24-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 38871/1993
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2589-023-0XPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1537 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-325-267A-2
Alignment Scores:
Pred. No.: 9,45e-08 Length: 1537
Score: 177.00 Matches: 112
Percent Similarity: 32.72% Conservative: 47
Best Local Similarity: 23.05% Mismatches: 181
Query Match: 7.71% Indels: 146
DB: 1 Gaps: 25
US-09-715-876-7_COPY_52_1296 (1-1245) x US-08-325-267A-2 (1-1537)
Qy 58 AATTATGCTTTAAAGGCCAGGA---TACCAACTTGGATGCTGTTGGTGGTCC 114
Db 104 AsnTrpGlyCysValGlyMetGlyAlaCysSerAsnSerGlnGlyIleAlaTyrTrpSer 123
Qy 115 TTAGAT-----GTTACAGTGCACATCCAGGGATACATTTCACATTGAAATATG----- 162
Db 124 ThrAspLeuPheGlyPheTyrThrThrProThrAsnVal---ThrLeuGluMetThrGly 142
Qy 163 -----CCATGTGTGTTTAAATATATACTACTTCAAA----- 192
Db 143 TyrPheLeuProGlnThrGlySerTyrThrPheLysPheAlaThrValAspAspSer 162
Qy 192 ----- 192

Db 163 AlaIleLeuSerValGlyGlyAlaThrAlaPheAsnCysCysAlaGlnGlnProPro 182
QY 193 ---ACATCTGTTGATTTAACTGCCGATGGTGTAA--- 225
Db 183 IleThrSerThrAsnPheThrIleAspGlyIleYsProTrpGlyGlySerLeuProPro 202
QY 226 -----TATGCTACTCTCAATTTATCTGGTGAAGAATTCACAACTTTTCTACATTA 279
Db 203 AsnIleGluGlyThrValTyrMetTyrAlaGlyTyrTyrProMet----- 218
QY 280 ACATGTAAGTGAACGCGCTTGAATATCCATTAAGGCATTTGGTACA----- 330
Db 219 -----LysValValTyrSerAsnAlaValSerTrpGlyThrLeuProIle 233
QY 331 ---GTTACTTTACCAATTTGCAATGTTGGTGAACAGGTTTCATCAACTGATTGGAA 387
Db 234 SerValThrLeuPro-----AspGlyThrThrValSerAspPheGlu 248
QY 388 GATTCTAAATGTTTTACTGCTGTGTACCAATACAGTCACATTAATGATGGTGATAAGAT 447
Db 249 Gly-----TyrValTyrSerPheAsp----- 256
QY 448 ATCTCAATGATGTTGATTTGAAAAGTCAACCGTT---GATCCAAGTCATATTTGTAT 504
Db 257 -----AspLeuSerGlnSerAsnCysThrValProAspProSerAsnTyrAla--- 272
QY 505 GCTTCCAGAGTTAGCCAGTCTCAATAAGGTCACAACTCTTTTGTGGCACCACAATGT 564
Db 273 ValSerThrThrThrThrThrThrGluProTrpThrGlyThrPheThrSerThr 292
QY 565 GAAATGTTTACACATCTGGTACAAATGGGTCTCCAGTAGTAGACGGTGTGCTATT 624
Db 293 GluMetThrThrValThrGlyThrAsnGlyValProThrAspGluThrValIleValIle 312
QY 625 GATTGCTCAATATTCATATTTGGTATATCAGAAAGGATTAATGATGGAAATATCCGGTT 684
Db 313 ArgThrProThrThrAlaSerThrIleThrThrThrGluProTrpAsnSerThrPhe 332
QY 685 TCATCTGAATCATTTAGTTACACTTAAACCTGATCACTAATGCAATTCAGATTAAATAT 744
Db 333 ThrSerThrSerThrGluLeuThrThrValThrGlyThrAsnGlyValArgThrAspGlu 352
QY 745 CAATAATGTACCTGCTGTTATCGTCCATTTATTGATGCTTATATTTCTGTACAGATGT 804
Db 353 ThrIleIle-----ValIleArgThrProThrThrAlaThrThrAla 366
QY 805 AACCAATATCTTTAGCATATACCAATGATATATCTTGTGCTGGCAGTCTCTGCAAGT 864
Db 367 IleThrThrThrGluProTrpAsnSerThrPheThrSerThrSerThrGluLeu----- 384
QY 865 AAACCTTTCTACTTTAAGTAGGCTGATCAAGAATAGTAGTCCGGATCTAACGGTATT 924
Db 385 -----ThrThrValThrGlyThrAsnGlyLeu 393
QY 925 -----GTCATTTGTGTACAACTAGAACAGTTACAGACAGTACCACTGTGTCACCT 975
Db 394 ProThrAspGluThrIleIleValIleArgThrProThrThrAlaThrThrAlaMetThr 413
QY 976 ACTTTA---CCATTCAATCCAGTGTGTGATAAACCAAAACA----- 1014
Db 414 ThrThrGlnProTrpAsnAspThrPheThrSerThrSerThrGluMetThrThrValThr 433
QY 1015 -----ATCGAAATTTTGCACACCTATTTCACACC 1041
Db 434 GlyThrAsnGlyLeuProThrAspGluThrIleIleValIleArgThrProThrThrAla 453
QY 1042 ACTACCATCACAACT-----TCATATGTTGGTGTGACTACTTCC 1080
Db 454 ThrThrAlaMetThrThrThrGlnProTrpAspAspThrPheThrSerThrSerThrGlu 473
QY 1081 TATCTGACTAAGACTGCA-----CCATTGGTGAACAGCTACTGTTATTGTT 1128
Db 474 MetThrThrValThrGlyThrAsnGlyLeuProThrAspGluThr-----IleIleValIle 492

QY 1129 GATGTGCCATATCATACTACCACA-----ACTGTTACCAGTGAATGGACAGGAACAATC 1182
Db 493 ArgThrProThrThrAlaThrThrAlaMetThrThrThrGlnProTrpAsnAspThrPhe 512
QY 1183 ACT-----ACCACCACAACCTCGTACCAAT-----CCAAGTGAATTC 1218
Db 513 ThrSerThrSerThrGluMetThrThrValThrGlyThrAsnGlyLeuProThrAsp--- 531
QY 1219 ATTGACACAGTGGTGGTA 1236
Db 532 ---GluThrIleIleVal 536

Search completed: September 8, 2005, 17:52:35
Job time : 60.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 8, 2005, 17:27:16 ; Search time 53 seconds

(without alignments)
4520.372 Million cell updates/sec

Title: US-09-715-876-7 COPY 52 1296

Perfect score: 2297

Sequence: 1 aagacaatcactggtgttt.....cagtgggtggtacaagttcca 1245

Scoring table: BLOSUM62

0.5	Xgapext	10.0	0.5
0.5	Ygapext	10.0	0.5
7.0	Fgapext	6.0	7.0
7.0	Delext	6.0	7.0

searched: 283416 seqs. 96216763 residues

Total number of bits satisfying chosen parameters: 566832

Minimum DB sec Length: 0

Minimum	DB seq	length:
Maximum	DB seq	length: 2000000000

Post-processing: Minimum Match 0%

Minimum	Match 0%
Maximum	Match 100%

Listing first 45 summaries

Command line parameters:

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Command: xane parafastx1
-MODEL=framedx nfp.model -DEV=xlp
-Q/cgna2/USSTO spool_gf09175876/runat_080920205 172227_18499/app_query.fasta_1.1415
-Ds=PIR -QFMT=fastan -SUFFIX=trp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRXI=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=oct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=DS09175876 @CGN 1.1.68 @runat_080920205 172227_18499 -NCPU=6 -ICPU=3
-NO MAP -LARGQUERY -NEG scores -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=1 -XGAEXT=0.5 -FGAPOP=6
-EGABYTES=7 -VgaPop=10 -VGAEXT=0.5 -DELOP=5 -DELEXT=7

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Database : PIR 79:★

: dir1: *

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pi1: *
pi2:
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p1r2: *
 p1r3: *

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: pir3: *
: pir4: *

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2186	95.2	1260	2	S60896	agglutinin-like pr
2	1903	82.8	1419	2	T30531	agglutinin-like ad
3	308.5	13.4	650	2	S22835	alpha-agglutinin -
4	198.5	8.6	948	2	T11678	hypothetical prote
5	177	7.7	1367	2	S51959	hypothetical prote
6	177	7.7	1537	2	S53465	floculation prote
7	176	7.7	1251	2	T21389	hypothetical prote
8	175.5	7.6	1832	2	T31113	mucin-like glycopr
9	174.5	7.6	973	2	T40778	hypothetical 129.5
10	171.5	7.5	456	2	T38221	hypothetical serin
11	167.5	7.3	682	2	A45155	mucin FIM-C.1 - Af
12	164	7.1	770	2	T22808	hypothetical prote
13	161.5	7.0	1075	2	S48992	floculation prote
14	161	7.0	1428	2	AC2324	hypothetical prote

ALIGNMENTS

RESULT 1

KE90J1 1
S60896
agglutinin-like protein - yeast (Candida albicans)

agglutinin-like protein = yeast (candida albicans)
C.Species: Candida albicans

C;species: Camilla arctica
C;Date: 27-Apr-1996 #sequence revision 13-Mar-1997 #text change 17-Mar-2000

C:Accession: S60896

R;Hoyer, L.L.; Scherer, S.; Shatzman, A.R.; Livi, G.P.

Mol. Microbiol. 15, 39-54, 1995

A;Title: Candida albicans ALS1: domains related to a Sa

A;Reference number: S60896; MUID:95272392; PMID:7752895

A; Accession: S60896

A; Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1260 <HOY>

A;Cross-references: EMBL:L25902; NID:g704426; PIDN:AAC41649.1; PID:g704427

C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase

Alignment Scores:		
Pred. No.:	1.9e-158	Length: 1260
Score:	2186.00	Matches: 415
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	95.17%	Indels: 0
DB:	2	Gaps: 0

750 00 715-875-7 COPY 53 1306 (1-1245) * S60896 (1-1260)

Qy	1	AAGCAATCACTGCTGTTTTTGAATAGTTTTTAATCAATTAACTGTGTGCCAATCTCTGCTAAT	60
Db	18	LysThrIleThrGlyValPheAspSerPheAsnSerLeuThrTrpSerAsnAlaAlaAsn	37
Qy	61	TATCTTTTCAAAGGCCGAGATACCCAACTTGGAAATGCTGTTTCGGTTGGTCCCTAGAT	120
Db	38	TyrAlaPheLysGlyProGlyTy-ProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp	57
Qy	121	GGTACCACTGCCAATCCAGGGGATACATTCAATTTGAATATGCCCATGTGTGTTTAAATAT	180
Db	58	GlyThrSerAlaAsnProGlyAspThrPheThrLeuAsnMetProCysValPheLysTyIyr	77

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QY 181 ACTACTTCACAAACATCTGTTGATTTAACTGCCGATGCTGTTAAATATGCTACTGTGCAA 240
Db 78 ThrThrSerGlnThrSerValAspLeuThrAlaAspGlyValIysThrAlaThrCysGln 97
QY 241 TTTTATTCTCGTGAAGAATTACAACTTTTCTACATTAAATGCTGTGAACGACGCT 300
Db 98 PheTyrSerGlyGluGluPheThrThrPheSerThrLeuThrCysThrValAsnAspAla 117
QY 301 TTGAATCATCCATTAAAGGATTTGGTACAGTTACTTACCAATTGCAATTCATGTTGGT 360
Db 118 LeuIysSerSerIleLysAlaPheGlyThrValThrLeuProIleAlaPheAsnValGly 137
QY 361 GGAACAGGTTCACTCAATGTTGGAAGATTTCTAAATGTTTACTGCTGTCACCAATACA 420
Db 138 GlyThrGlySerThrAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
QY 421 GTCCATTTAATGATGGTGATAAGATATCTCAATTGATGTTGAGTTGAAAAGTCAACC 480
Db 158 ValThrPheAsnAspGlyAspLysAspIleSerIleAspValGluPheGluLysSerThr 177
QY 481 GTTGATCCAAAGTCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGTCACA 540
Db 178 ValAspProSerAlaTyrLeuTyrAlaSerArgValMetProSerLeuAsnLysValThr 197
QY 541 ACTCTTTTGTGGCACCACCAATGTTGAAAATGGTTACACATCTGTTCAATGGGGTCTCC 600
Db 198 ThrLeuPheValAlaProGlnCysGluAsnGlyTyrThrSerGlyThrMetGlyPheSer 217
QY 601 AGTAGTAACGGTGCATTTGCTATTTGATTTGCTCAAAATATTCATATGTTGATTCACAAAGGA 660
Db 218 SerSerAsnGlyAspValAlaIleAspCysSerAsnIleHisIleGlyIleThrLysGly 237
QY 661 TTAATGATGGAATTAATCCGGTTTCATCTGCAATCATTTAGTTACACTAAACTGTGACA 720
Db 238 LeuAsnAspTrpAsnTyrProValSerSerGluSerPheSerTyrThrLysThrCysThr 257
QY 721 TCTAATCGAATTCAGATTAATAATCAAAATGTACTCTGTTATCTGTTATCTCCATTTATGAT 780
Db 258 SerAsnGlyIleGlnIleLysTyrGlnAsnValProAlaGlyTyrArgProPheIleAsp 277
QY 781 GCTTATATTTCTGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGATATACT 840
Db 278 AlaTyrIleSerAlaThrAspValAsnGlnTyrThrLeuAlaTyrThrAsnAspTyrThr 297
QY 841 TGTCTGGCAGTCTGTCGAAGTAAACCTTTCACTTTTAAGATGGAGCTGGATACAAAGAT 900
Db 298 CysAlaGlySerArgLeuGlnSerLysProPheThrLeuArgTrpThrGlyTyrLysAsn 317
QY 901 AGTCATGCCGATCTAACGGTATTGTCATTTGTTGCTACAACTAGAAACAGTTACAGACAGT 960
Db 318 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 337
QY 961 ACCACTGCTGCTACTTTACCATTCATCCAAAGTGTGATAAACCAAAACAAATCGAA 1020
Db 338 ThrThrAlaValThrThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu 357
QY 1021 ATTTTGCACTTATCCAACTACCATTCACACTTCATATGTTGGTGGTGCATCTTCC 1080
Db 358 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 377
QY 1081 TATCTGATAGACTGACCAAAATTTGGTGAACACAGTACTGTTATTTGTTGATGTGCCATAT 1140
Db 378 TyrLeuThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 397
QY 1141 CATACTACCAACTGTTTACAGTGAATGGACAGGAACAATCATCTACCAACCACTCGT 1200
Db 398 HisThrThrThrThrValThrSerGluTrpThrGlyThrIleThrThrThrThrArg 417
QY 1201 ACCAATCCAACTGATTCAAATTTGACACAGTGGTGTGACAAAGTTCCA 1245
Db 418 ThrAsnProThrAspSerIleAspThrValValGlnValPro 432
```

```
RESULT 2
T30531
agglutinin-like adhesin - Yeast (Candida albicans)
C;Species: Candida albicans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30531
R;Gaur, N.K.; Klotz, S.A.
Infect. Immun. 65, 5289-5294, 1997
A;Title: Expression, cloning, and characterization of a Candida albicans gene, ALA1, th
A;Reference number: Z20847, WUID:98053977, PMID:9393828
A;Accession: T30531
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1419 <GAU>
A;Cross-references: UNIPROT:O13368, EMBL:AF025429, NID:g2522218, PID:g2522219, PIDN:AA8
C;Genetics:
A;Gene: ALA1
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
Alignment Scores: 6.51e-137 Length: 1419
Pred. No.: 1903.00 Matches: 358
Score: 91.33% Conservative: 21
Percent Similarity: 86.27% Mismatches: 36
Best Local Similarity: 82.85% Indels: 0
Query Match: 2 Gaps: 0
DB:
US-09-715-876-7_COPY_52_1296 (1-1245) x T30531 (1-1419)
QY 1 AGACAATCACTGCTGTTTGTGATGTTTAAATTAATCACTTGGTCCATGCTGCTAAT 60
Db 18 LysAlaIleThrGlyIlePheAsnSerIleAspSerLeuThrTrpSerAsnAlaGlyAsn 37
QY 61 TATGCTTTCAAAAGGGCCAGATACCCAACTTGGAATGCTGTTTGGTGGTCTTAGAT 120
Db 38 TyrAlaPheLysGlyProGlyTyrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57
QY 121 GGTACAGTCCCAATCCAGGGATACATTCACATTCGAATATGCATGTGTGTTAAATAT 180
Db 58 GlyThrSerAlaAsnProGlyAspThrPheIleLeuAsnMetProCysValPheLysPhe 77
QY 181 ACTACTTCACAAACATCTGTTGATTTAACTGCCGATGCTGTTAAATATGCTACTGTCAC 240
Db 78 ThrAlaSerGlnLysSerValAspLeuThrAlaAspGlyValIysTyrAlaThrCysGln 97
QY 241 TTTTATTCTGTCGAAGAATTACAACTTTTCTCATTAACATGATGTGTAACGACGCT 300
Db 98 PheTyrSerGlyGluGluPheThrThrPheSerSerLeuLysCysThrValAsnAsn 117
QY 301 TTGAATCATCCATTAAAGGATTTGGTACAGTTACTTTCACCAATGCAATTCATGTTGGT 360
Db 118 LeuArgSerSerIleLysAlaLeuGlyThrValThrLeuProIleAlaPheAsnValGly 137
QY 361 GGAACAGGTTCACTGATTTGGAAGATTTCTAAATGTTTACTGCTGTCACCAATACA 420
Db 138 GlyThrGlySerSerValAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
QY 421 GTCCATTTAATGATGGTGATAAGATATCTCAATTGATGTTGAGTTGAAAAGTCAACC 480
Db 158 ValThrPheAsnAspGlySerLysLysLeuSerIleAlaValAsnPheGluLysSerThr 177
QY 481 GTTGATCCAAAGTCATATTTGTATGCTCCAGAGTTATGCCAAGTCTCAATAAGTCCACA 540
Db 178 ValAspGlnSerGlyTyrLeuThrThrSerArgPheMetProSerLeuAsnLysIleAla 197
QY 541 ACTCTTTTGTGGCACCACCAATGTTGAAAATGGTTACACATCTGTCGTCAAATGGGTTCTCC 600
Db 198 ThrLeuTyrValAlaProGlnCysGluAsnGlyTyrThrSerGlyThrMetGlyPheSer 217
QY 601 AGTAGTAACGGTGCATTTGCTATTTGATGTTGCTCAAAATATTCATATGTTGATTCACAAAGGA 660
Db 218 ThrSerTyrGlyAspValAlaIleAspCysSerAsnValHisIleGlyIleSerLysGly 237
```


submitted to the EMBL Data Library, February 1994
A:Description: Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of the 5
A:Reference number: S53458
A:Accession: S53465
A:Molecule type: DNA
A:Residues: 1-1537 <BUS>
A:Cross-references: UNIPROT:P32768; EMBL:L28920; NID:q1616966; PIDN:AAC09499.1; PID:G694
R:Watarai, J.; Takata, Y.; Ogawa, M.; Sahara, H.; Koshino, S.; Onneta, M.L.; Airaksinen,
Yeast 10, 211-225, 1994
A:Title: Molecular cloning and analysis of the yeast flocculation gene FLO1.
A:Reference number: S43543; MUID:9426325; PMID:8203162
A:Accession: S43543
A:Molecule type: DNA
A:Residues: 1-428, 'M', 430-473, 'M', 475-518, 'M', 520-549, 'T', 551-608, 'L', 610-636, 'M', 638-659
A:Cross-references: EMBL:X78160

K:Omura, M.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: S57851
 A:Accession: S57851
 A:Molecule type: DNA
 A:Residues: 1-428, 'M', 430-463, 'D', 465-473, 'M', 475-518, 'M', 520-549, 'T', 551-608, 'L', 610-633
 A:Cross-references: EMBL:X78160; NID:G535933; PIDN:CA55024.1; PID:G535934
 F:Teunissen, A.W.R.H.; Holub, E.; van der Hucht, J.; van den Berg, J.A.; Steensma, H.Y.
 Yeast 9, 423-427, 1993
 A:Title: Sequence of the open reading frame of the FLO1 gene from *Saccharomyces cerevisiae*
 A:Reference number: S31230; MUID:93289821; PMID:8511970
 A:Accession: S31230
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-296, 927-1516, 'TAYWPVVV' <TEU>
 R:Bidard, F.; Bony, M.; Blondin, B.; Dequin, S.; Barre, P.
 Yeast 11, 809-822, 1995
 A:Title: The *Saccharomyces cerevisiae* FLO1 flocculation gene encodes for a cell surface
 A:Reference number: S57349; MUID:96090130; PMID:7483845
 A:Accession: S57349
 A:Molecule type: DNA
 A:Residues: 1243-1274; 1308-1339; 1359-1390 <BID>
 C:Genetics:
 A:Gene: SGD:FLO1
 A:Cross-references: SGD:S0000084; MIPS:YAR050W
 A:Map position: 1R
 C:Keywords: duplication; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-1537/Product: flocculation protein FLO1 #status predicted <MAT>
 F:953-997/Domain: repeat A2 <RA2>
 F:998-1042/Domain: repeat A3 <RA3>
 F:1043-1081/Domain: repeat A4 <RA4>
 F:1226-1276/Domain: repeat B1 <RB1>
 F:1277-1284/Domain: repeat B2 (partial) #status atypical <RB2>
 F:1291-1341/Domain: repeat B3 <RB3>
 F:1342-1392/Domain: repeat B4 <RB4>
 F:1408-1416/Domain: repeat C1 <RC1>
 F:1417-1425/Domain: repeat C2 <RC2>
 F:1426-1434/Domain: repeat C3 <RC3>
 F:135, 187, 262, 1114/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Alignment Scores:
Pred. No.:      1.35e-05      Length:      1537
Score:          177.00      Matches:      112
Percent Similarity: 32.72%      Conservative: 47
Best Local Similarity: 23.05%      Mismatches: 181
Query Match:      7.71%      Indels:      146
DB:              2      Gaps:      25

US-09-715-876-7_COPY_52_1296 (1-1245) x S53465 (1-1537)

Qy  58  AATTATGCTTTTCAAAAGGCCACAGGA---TACCACCACTTGGAAATGCTGTTTGGTGTGTC 114
      |||:|||||
Db  104  AsnTrpGlyCysLysGlyMetGlyAlaCysSerAsnSerGlnGlyIleAlaTyTrpSer 123
      |||:|||||

Qy  115  TTAGAT-----GGTACCAGTGGCCCAATCCAGGGGATACATTCACATTGAATATG----- 162
      |||
Db  124  ThrAspLeuPheGlyPheTyThrTrpProThrAsnVal---ThrLeuGluMetThrGly 142
      |||

```


QY 1042 ACTACCATCAAACT-----TCATATGTTGGTGGTACTACTTCC 1080
||||| ||| : : : : :
Db 454 ThrThrAlaMetThrThrGlnProThrAsnAspThrPheThrSerThrGlu 473
QY 1081 TATCTGAATAGACTGCA-----CCAATGGTGAACAGCTACTGTTATTGTT 1128
||||| ||| : : : : :
Db 474 LeuThrThrValThrGlyThrAsnGlyLeuProThrAspGluThr---IleIleValIle 492
QY 1129 GATGGCCATATCATACACACA-----ACTGTTACCACTGAATGCACAGGAACAATC 1182
||||| ||| : : : : :
Db 493 ArgThrProThrThrAlaThrThrAlaMetThrThrGlnProThrAsnAspThrPhe 512
QY 1183 ACT-----ACCACCACTCTGTACCAAT-----CCAATGATTCA 1218
||||| ||| : : : : :
Db 513 ThrSerThrSerThrGluIleThrThrValThrGlyThrAsnGlyLeuProThrAsp--- 531
QY 1219 ATTGACACAGTGGTGA 1236
: : : : :
Db 532 ---GluThrIleIleVal 536

RESULT 7

T21389

hypoetical protein F26C11.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21389

R:Matthews, P.

submitted to the EMBL Data Library, December 1994

A:Reference number: Z19416

A:Accession: T21389

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1251 <WIL>

A:Cross-references: UNIPROT:Q09550; EMBL:Z47072; PIDN:CAA87369.1; GSPDB:GN00020; CESP:F2

A:Experimental source: clone F26C11

C:Genetics:

A:Gene: CESP:F26C11.3

A:Map position: 2

A:Introns: 24/1; 111/1; 208/1; 272/1; 380/1; 394/3; 485/3; 586/3; 630/3; 669/3; 713/3; 7

Alignment Scores:

Pred. No.:	1.58e-05	Length:	1251
Score:	176.00	Matches:	112
Percent Similarity:	37.83%	Conservative:	62
Best local Similarity:	24.35%	Mismatches:	156
Query Match:	7.66%	Indels:	130
DB:	2	Gaps:	23

US-09-715-876-7_COPY_52_1296 (1-1245) x T21389 (1-1251)

QY 76 CCAGATACCCAACTTGAATGCTGTTGGTGGTCTTAGATGGTACCAGT----- 129
||||| ||| : : : : :
Db 609 ProGlyThrThrThrTyAsn-----TrpProThrGlyThrThrArgMet 624
QY 130 -----GCCAATCCAGGGGATACATC 150
||||| ||| : : : : :
Db 625 LeuProSerGlyGluIleIleLeuSerGluSerLeuIleAlaTyProAsnCysThr--- 643
QY 151 ACATTGAATATGCCATGTGTGTTAAATATACTACTTACAAACATCTGTTGATTAACT 210
||||| ||| : : : : :
Db 644 ThrValLeuMetGlnLeuIleTyThrProSerThrAsnLysThrArgThrGluThrThr 663
QY 211 GCCGAT-----GGTGTAAATATGCTACTGTCTCAATTTTATTCTGGTGAAGATTCACA 264
||||| ||| : : : : :
Db 664 ThrAspThrGluGlyCysLysLysThrSerThrIleSerSerSerSerSerLysPheSer 683
QY 265 -----ACTTTTCTACATTAAACATGCTACTGTGAAC----- 294
||||| ||| : : : : :
Db 684 IleThrProThrProThrProSerSerGlyThrThrThrTyAsnTrpProThrGlyGly 703
QY 295 -----GACGCTTTGAAATCATCCATTAAAGCATTT--- 324
||||| ||| : : : : :
Db 704 ThrThrArgThrLeuProSerGlyGluIleIleLeuSerGluSerLeuIleAlaPheGln 723

RESULT 8

T31113

mucin-like glycoprotein 900 - Cryptosporidium parvum

C:Species: Cryptosporidium parvum

QY 325 -----GGTACAGTTACTTTACCAATTCATTCATGTTGGTGGAAACAGGTTTCATCACT 378
||||| ||| : : : : :
Db 724 AsnCysThrThrValLeuMetGlnLeuIleTyAsn-----ProSerThr 738
QY 379 GATTGGGAAGATCTTAATGTTTTTACTGCTGGTACCAATACAGTCACATTAATGATGGT 438
: : : ||| : : : : :
Db 739 Asn-----LysThrArgThrGluThrThrAspAlaGluGly 751
QY 439 GATAAAGATATCTCAATTTGATGTTGAGTTTGAAGAAGTCAACCGTTGATCCAAGTGCAAT 498
||||| ||| : : : : :
Db 752 CysLysLysThrSerSerThrSerLysIleSerThrThrProThrSerProThr----- 769
QY 499 TTGTATGCTTCCAGAGTTATGCCAAGTTCATTAAGGTCAACAATCTTTTGTGGGCCACA 558
||||| ||| : : : : :
Db 770 -----SerSerLysProThrProThrSerSerMetThrThrTyAsnTrpPro 787
QY 559 CAATGTGAAATGTTACACATCTGGTACATGAGGGGTTCTCCAGTAGTAGGAGGTCAGTT 618
: : : ||| : : : : :
Db 788 -----ThrGlyGlyThrThrArgThrLeu-----ProSerGlyGluIle 800
QY 619 GCTATTGATTGCTCAAAATATTCATATTGGTATCACAAAAGGATTAATGATTGAATAT 678
800 ----- 800
QY 679 CCGGTTTCATCTGAATCATTTAGTTTACACTAAACCTTTGTATCATCTAATGGAATTCAGATT 738
: : : ||| : : : : :
Db 801 ---IleLeuSerGluSerLeuIleAlaTyLysAsnCysThrThrValLeuMetGlnLeu 819
QY 739 AAATATCAAAATGATCTGCTGGTTATCGTCCATTTATGATGTTATATTTCTGCTACA 798
||||| ||| : : : : :
Db 820 IleTyAsn-----ProSerThrAsnLysThrArgThrGlu-----ThrThrThr 834
QY 799 GATGTTAAC-----CAATATCTTTAGCATATACCAATGATTATATCTTTGCTGGCAGT 852
||||| ||| : : : : :
Db 835 AspAlaGlnGlyCysLysAlaThrSerSerThrSerLeuLysProThrSerProSerSer 854
QY 853 CGTCTGCAAAAGTAAACCT---TTCACTTTTAAGATGG---ACTGGATACAAGAATAGTCAAT 906
||||| ||| : : : : :
Db 855 SerThrAlaSerProProThrThrThrTyAsnTrpProThrGlyGlyThrThrArgThr 874
QY 907 GCGGATCTAACGGTATTGTTCATTTGCTGCTACAACTAGACAGTTACAGACAGTACCACCT 966
||||| ||| : : : : :
Db 875 LeuProSerGlyGluIleIleLeuSerGluSerLeuIleAlaTyLysAsnCysThrThr 894
QY 967 GCTGTCATCTACTTTACCATTCATCCCAAGTGTGATAAACCAACAAACA----- 1014
: : : ||| : : : : :
Db 895 ValLeuMetGlnLeuIleTyAsnProSerThrAsnLysThrArgThrGluThrThrThr 914
QY 1015 -----ATCGAAATTTTGCACACTATTCCAACTTCCAACTTCCAACTTCCAACT 1056
||||| ||| : : : : :
Db 915 AspAlaGlnGlyCysLysAlaThrIleThrThrProThrPro-----IleThrThr 931
QY 1057 TCATATGTTGGTGGTACTTCTCTATCTGCTAAGACTGCACCAATTTGGTGA----- 1110
: : : ||| : : : : :
Db 932 ThrTy---AsnTrpProThrGlyGlyThrThrArgThrLeuProSerGlyGluIleIle 950
QY 1111 -----ACAGCTACTGTTATTTGTTGATGTCATAT 1140
||||| ||| : : : : :
Db 951 LeuSerGluSerLeuIleAlaTyLysAsnCysThrThrValLeuMetGlnLeuIleTy 970
QY 1141 CAT-----ACTACCACCAACTGTTTACCAGTGAATGGACAGGAAACAACTCACT 1185
: : : ||| : : : : :
Db 971 AsnProSerThrAsnLysThrArgThrGluThrThrSerAspAlaGlnGlyCysLysAla 990
QY 1186 ACCACCACTCTGCTACCAATCCAACTGATTCAATGACACAGCTGGTGGTCAAGT 1241
||||| ||| : : : : :
Db 991 ThrSerThrThrGlnThrProThrThr---PheAsnTrpProThrGlyGlyThrThr 1008

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31113
R;Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, P.; Dubremet
Mol. Biochem. Parasitol. 95, 93-110, 1998
A;Title: A novel multi-domain mucin-like glycoprotein of *Cryptosporidium parvum* mediates
A;Reference number: Z20989; MUID:99066935; PMID:9851610
A;Accession: T31113
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1832 <BAR>
A;Cross-references: UNIPROT:O96503; EMBL:AF068065; NID:94063041; PID:94063042; PIDN:AAC9

Alignment Scores:		
Pred. No.:	1.77e-05	Length:
Score:	175.50	Matches:
Percent Similarity:	33.91%	Conservative:
Best Local Similarity:	22.88%	Mismatches:
Query Match:	7.64%	Indels:
DB:	2	Gaps:

US-09-715-876-7 COPY 52 1296 (1-1245) x T31113 (1-1832)

[illegible]

RESULT 9

T40778
hypothetical 129.5 kd protein - fission yeast (*Schizosaccharomyces pombe*)
C/Species: *Schizosaccharomyces pombe*
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C/Accession: T40778
R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, February 1998
A/Reference number: Z21884
A/Accession: T40778
A/Status: preliminary; translated from GH/EMBL/DDEJ
A/Molecule type: DNA
A/Residues: 1-973 <LVN>
A/Cross-references: EMBL:AL021837; PIDN:CAAL17032.1; GSPDB:GN00067; SPDB:SPBC947.04
A/Experimental source: strain 972h-; cosmid c947
C/Genetics:
A/Gene: SPDB:SPBC947.04
A/Map position: 2

Alignment Scores:		
Pred. No.:	2.02e-05	Length:
Score:	174.50	Matches:
Percent Similarity:	35.35%	Conservative:
Best Local Similarity:	22.63%	Mismatches:
Query Match:	7.60%	Indels:
DR:	2	Gaps:
		25
		973

US-09-715-876-7 COPY 52 1296 (1-1245) X T40778 (1-973)

Qy	40	ACTTGGTCCAA	TGCTGCTAA	TATATGCTTT	CAAAGGGCC	GAGGATAC	CCCAACTTGG	AATGCT	99
Db	149	ThrTpsrThr	AsnLeu	-----	-----	ProThrAsn	ProThrThr	Ala	162
Qy	100	GTTTGGGTGG	TCTCTAGAT	GTGACAGT	GCCCAATC	CCGGGATAC	ATTCACAT	TGAAT	159
		:::	:::	:::	:::	:::	:::	:::	
Db	163	Ile-----	TyrSerThr	SerGlySer	-----	-----	AsnIle	Thr	173
Qy	160	ATGCATGTGT	GTGTTAAAT	AATATACT	ACTTCTACA	CAACATCT	GT---GATT	TAAC	216
			:::	:::					
Db	174	ThrProTyr	SerAsnArg	IleThrAsn	SerAsnThr	SerValAsn	AspIleThr	SerLys	193
			:::	:::					


```
QY 379 GATTGTGGAAGATCTCTAAATGTTTACTGCTGGTACCAATACAGTCACATTTAATGATGGT 438
Db   :|||
QY 207 MetileProSerSerSerPheThrThrThrThrGlySerProTyrTyrAsnThrSer 226
Db   :|||
QY 439 GATAAAGATATCTCAATTGATGTTGATGTTGAAAGTCAACCGTTGATGCAAGTGCAATAT 498
Db   :|||
QY 227 -----SerPheLeuProSerSerValIleSerSerAlaSer 238
QY 499 TTGTATGCTTCCAGAGTTATGCCA----- 522
Db   :|||
QY 239 LeuSerSerSerSerValLeuProThrSerSerIleIleThrSerThrSerThrProValThr 258
QY 523 -----ACTCTCAATAAGGTCACCAACTCTTTTCTGGTGGCACCACCAATGTGAAAT 570
Db   :|||
QY 259 ValSerSerSerSerLeuSerSerPheThrProSerTyrSerThrAsnLeuThrThrThr 278
QY 571 GGTGTACATCTGTGTACAAATGGGTTCTCCAGTAGTAGTAACGGTGACGGTGTCTATTGATGC 630
Db   :|||
QY 279 GlySerThrThrThrGlySerAlaThrValSerSerSerProPheTyrSerAsnSer 298
QY 631 TCRAATATTCATATTTGTTATCACAAAAGGATTAAATGATTGGAATTATCCGGTTTCACT 690
Db   :|||
QY 299 SerValIleProThrSerValProSerSerValSerSerPhe-----ThrSer 314
QY 691 GAATCATTTTGTACATCAAACTTTGTACATCTAATGGAATTCAGATTAAATATCAAAAT 750
Db   :|||
QY 315 SerSerSerSerTyrThrThrThrLeuThrAlaSerAsnThrSerValThrTyrThrGly 334
QY 751 GTACCTGCTGTTATCGTCATTTATTGATGCTTATATTTCTGCTACAGATGTTAACCA 810
Db   :|||
QY 335 ThrGlyThrGly-----SerAlaThr----- 341
QY 811 TATACTTTAGCA-----TATACCAATGATTAT-----ACTTGTGCTGGCAGT 852
Db   :|||
QY 342 PheThrSerSerProProPheTyrSerAsnSerSerValIleProThrSerValProSer 361
QY 853 CGTCTGCAAGTAAACCTTTTCACTTTAAGATGGAATGATGATAGTATGATGCGGA 912
Db   :|||
QY 362 SerValSerSer-----PheThrSerSerAsnSerSerTyrThrThrLeuThrAla 379
QY 913 TCTAACGGTATGTGTCATTTGTTGTCACAACTAGACAGTACAGTACAGTACAGTGTGTC 972
Db   :|||
QY 380 SerAsn-----ThrSerIleTyrThrGlyThrGlyThrGlySerAlaThrPheThr 397
QY 973 ACTACTTTACCATTC-----AATCCAAGTGTGATATAAAACCAACCAATCGAAATTTG 1026
Db   :|||
QY 398 SerSerProProPheTyrSerAsnSerSerVal----- 408
QY 1027 CAACCTATTCCCAACCACT-----ACCATCAACACTTCATATGTTGTTGACTACTTCC 1080
Db   :|||
QY 409 -----IleProThrSerValProSerSerValSerSerPheThrSerSerAsnSerSer 426
QY 1081 TATCTGACTAAGACTGCACCAATTTGGTGAACACACTACTGTTATTGTTGATGTCATAT 1140
Db   :|||
QY 427 TyrThrThr-----ThrLeuThrAla----- 433
QY 1141 CATACTACCACAACTGTTTACCAGTGAATGGACAGCAACAATCACTACACCAACACTCGT 1200
Db   :|||
QY 434 ---SerAsnThrThrValThrPheThrGlyThrGlyThrGlySerAlaThrPheThrSer 452
QY 1201 ACCAATCCA 1209
Db   :|||
QY 453 SerProPro 455
```

RESULT 11

A45155
mucin FIM-C.1 - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: A45155
R:Hauser, F.; Hoffmann, W.
J. Biol. Chem. 267, 24620-24624, 1992
A:Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1)

A:Reference number: A45155; MUID:93077556; PMID:1447205
A:Accession: A45155
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-662 <HAU>
A:Cross-references: UNIPROT:Q05049; GB:L02115; NID:g214147; PIDN:AAA74725.1; PID:g95146
F:162-202/Domain: trefoil homology <TRF1>
F:307-347/Domain: trefoil homology <TRF2>
F:354-394/Domain: trefoil homology <TRF3>
F:526-566/Domain: trefoil homology <TRF4>
F:573-613/Domain: trefoil homology <TRF5>
F:621-661/Domain: trefoil homology <TRF6>

Alignment Scores:
Pred. No.: 6.68e-05 Length: 662
Score: 167.50 Matches: 94
Percent Similarity: 31.52% Conservative: 28
Best Local Similarity: 24.29% Mismatches: 166
Query Match: 7.29% Indels: 99
DB: 2 Gaps: 16

US-09-715-876-7_COPY_52_1296 (1-1245) x A45155 (1-662)

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QY 121 GGTACAGTCCCATCCAGGGATACATTCACATTCGAATATGCCATGTGTAAATAT 180
Db   :|||
QY 206 GlyHisSerHisGluHisThrThrThrThrLysAlaProThrThrLysGlnIle 225
QY 181 ACTACTTCCAAACATCTGTGATTTAACTGCCGATGGTGAATATGCTACTCTGTC 240
Db   :|||
QY 226 AlaThrThrThrThrThrProThrThrThrThrThrThrLys----- 240
QY 241 TTTTATCTGCTGGAAGAATTCACAACTTTTCTACATTAACATGTACTGTGAACGCGT 300
Db   :|||
QY 241 -----AlaThrProThrThrThrThrThrLysAlaThrProThr 254
QY 301 TTGAATCATTCATTAAGCATTTGGTACAGTTACTTTACCAATTCATTCATGTGGT 360
Db   :|||
QY 255 ThrThrThrThrLysAlaThrThrThrThrThrPro----- 268
QY 361 GGAACAGGTTCACTCACTGATTTGGAAGATTTCTAAATGTTTACTGCTGTACCAAT 420
Db   :|||
QY 269 -----ThrThrThrThrThrThrLysAlaThrThrThrProThrThrThr 284
QY 421 GTCACATTTAATGATGGTGATAAAGATATCTCAATTGATGTGGAGTTGAAAGTCAAC 480
Db   :|||
QY 285 -----ThrThr----- 286
QY 481 GTTGATCCAGTGCAATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAGGTCACA 540
Db   :|||
QY 287 ThrThrProThrThr-----ThrThrThrLysAlaThr 297
QY 541 ACTCTTTTGTGGCACCACAAATGTGAAATGGTTACACATCTGGTACAAATGGGGTCTCC 600
Db   :|||
QY 298 ThrThrThrThr-----ThrSerGlyGluCysLysMetGlu 310
QY 601 AGTAGTAACGGTGAACGTTGCTATTGATGCTCAAAATATTCATATGTTGATCAAAAGGA 660
Db   :|||
QY 311 ProSerLysArgGlu-----AspCysGly-----TyrSerGlyIleThrGluSer 325
QY 661 TTAATGATGGAATTTATCCGGTTTCACTCGAATCATTTAGTTACACTAAACTGTGACA 720
Db   :|||
QY 326 GlnCysArgThrLysGlyCysCysPheAspSerSerIleProGlnThrLysTrpCysPhe 345
QY 721 TCTAATGGAATTCAGATT-----AAATATCAAAATGTACCTGTGCTGT 762
Db   :|||
QY 346 TyrThrLeuSerGlnValAlaAspCysLysValGluProSerGlnArgValAspCysGly 365
QY 763 TATCGTCAATTTATGATGCTTATATTTCTGCTACAGATGTTAACCAATATATCTTAGCA 822
Db   :|||
QY 366 PheArgGly-----IleThrAlaAspGlnCysArgGlnLysAsnCysCys 380
QY 823 TATACCAATGATTTACTTGTGCTGCAGCTCGTCTGCAAGTAGTAACCTTTCACCTTTAAGA 882
Db   :|||
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Db 381 Phe-----AspSerSerIleSerGlyThr-----Lys 389
QY 883 TGGACTGATACAGAATAGTAGTCCGGATCTAACGGTATTCATGTTGCTACAACT 942
Db 390 TrpCysPheTyrSerThrSerGln-----ValAlaAlaThr 401
QY 943 AGAACAGTTACAGACAGPACCACTGCTGCTACTACTTTACCAATTCATCAAGTGTGAT 1002
Db 402 LysThrThrThrThrThrThrThr-----ThrThrThrThrThrThrThrThr 419
QY 1003 AAA-----ACCAAAACAATCGAAATTTGGCAACTATTCACCACTACCAC 1050
Db 420 LysAlaThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 439
QY 1051 ACAACTTCATATGTTGGTGTGACTACTTCCTATCTGCTAAGACTGCACCAATGGTGAA 1110
Db 440 ThrThrThr-----ThrLysAlaThrThrThrThrThrThrThrThrThrThr 458
QY 1111 ACAGCTACTGTTATGTTGATGTGCCATATCATCTACTACCAACTGTTACCAGTAATGG 1170
Db 459 ThrThrLysAlaThrThrThrThrThrThrThrThrThrThrThrThrThrThr 478
QY 1171 ACAGGAACAATCACTACC-----ACCACAACCTGTCACCAATCCAACTGATTC 1224
Db 479 ThrLysAlaThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 498
QY 1225 ACAGTGGGTGACAAAGTTCCA 1245
Db 499 LysAlaThrThrThrThrPro 505

RESULT 12
hypochemical protein F56H9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22808
R:Burton, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19618
A:Accession: T22808
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-770 <WIL>
A:Cross-references: UNIPROT:Q20908; EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:FS
A:Experimental source: clone F56H9
C:Genetics:
A:Gene: CESP:F56H9.1
A:Map position: 5
A:Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2

Alignment Scores:
Pred. No.: 0.000125 Length: 770
Score: 164.00 Matches: 104
Percent Similarity: 35.60% Conservative: 58
Best Local Similarity: 22.86% Mismatches: 144
Query Match: 7.14% Indels: 149
DB: 2 Gaps: 20

US-09-715-876-7_COPY_52_1296 (1-1245) x T22808 (1-770)
QY 16 GTTTTGTAGTTTAAATTCATTAACCTGGTCCAAATGCTGCTAATATGCTTTCAAAGGG 75
Db 295 IlePheAspValPheAsn-----GlnProAlaGluAsnGlnGlyPhe----- 308
QY 76 CCAGGATACCCAACTGGAACTGCTGTTTGGTGGTCTCTAGATGGTACCAGTGCCAAAT 135
Db 309 ProGlnSerValThrValAsnAlaGlnCys----- 318
QY 136 CCAGGGGATACATTCACATATGCAATATGCAATGCTGTTGTTAAATATFACTTTCACAAACA 195
Db 319 -----AsnArgIleLeuIleAsnLeuPheMetPhePheLysPhe----- 331
QY 196 TCTGTTGATTTAACTGCCGAGGTGTTAAATATGCTACTTGTTCATTTATTTCTGGTGAA 255
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Db 332 -----LeuSerTyrGluLysThrSerPheTyr----- 340
QY 256 GAATTCACAACCTTTTCTACATTAACATGTACTGTGAACCGCTTTGAATCATCATTCAT 315
Db 341 -----IleLeuCysThrSerLys-ThrLeuSerAsnPheIleLe 353
QY 316 AAGGCATTTG-----GTACAGTTACTTTTAC---CAATTGCAATTC 351
Db 353 uLeuThrValTyrPheLeuTyrIleGlyProThrGluLeuLeuTyrThrGlnIleGlySe 373
QY 352 AATG-----TGGTGGGAACA 366
Db 373 rMetAsnLeuAsnThrTyrLeuAsnGlnThrMetGlyLeuGlyMetTyrLeuGlnGlyPr 393
QY 367 GGTTCATCACTGATTTGGAAGATTTCTAATGTTTACTGCTG----- 409
Db 393 oIleThrGlnMetIleIleThrIleAsnArgPheLeuValIleIleTrpPheThrProThrHi 413
QY 410 -GTACCAATACAGTCACATTTAATGATGGTG-----ATAAGATATCTCAATGTGAT 462
Db 413 sValProGlnTyrSerHisArgIleThrLeuGlyAlaLeuSerValSerTrpIleThrVa 433
QY 463 GAGTTTGAAAGTCAACCGTTGATCCAAAGTGCATATTTGTATGCTTCCAGATTA----- 517
Db 433 lThrTrpLeuSerThr-----LeuIleGlyLeuProGlyPheAspAs 447
QY 518 -----TGCCAAGTCTCAATAGGTCACA 540
Db 447 nAsnAsnAsnPheAspIleIleIleAsnLeuAlaAsnCysArgValProIleGlyPheGl 467
QY 541 ACTCTTTTCTGGCACCACACAATGTGAAATGGTTACACATCTGTGTAACATGGGTCTCC 600
Db 467 u-----HisIleGlyTyrTyrSerThrPr 475
QY 601 AGTAGTAACG---GTGACGTTGCTATTGATTTGCTCAAAATTTCAATATTTGTTATCACA 657
Db 475 oCysAsnAsnGlnIleThrIleIleValSerGlyIlePhe----- 489
QY 658 GGAATTAATGATTTGGAATATTCGGTTTCATCTGTAATCATTTAGTTACATAAACTTGT 717
Db 490 -----LeuIleGlyPheLeuThrAsnPheMetAsnPheMetIleGlyGlyLysLeuIl 507
QY 718 ACAT-----CTAATGGAATTCAGATTAATATAATACAA-----AT 750
Db 507 eTyrThrTrpLysThrLeuThrIlePheArgPheLeuSerAsnPheLysCysValMetLy 527
QY 751 GTACCTGCTGTTATCGTCATTTATTGATGCTTATATTCTGCTCAGATGTTTAACCAA 810
Db 527 sTrpIleSerThrLeuLeuHisIleLeuLeuLeuThrTyrLysLeu--AspValIleAsn 546
QY 811 TATACCTTTAGCATATACCAATGATATATCTTGTGCTGCGAGTCTGCTGCAAGTAACCT 870
Db 547 -----SerCysIleAlaThrSerProThrAlaAspPro 557
QY 871 TTCATTTTAAGATGGACTGGATACAAAGTAGTATGATCCGGATCTAACGGTATTGTCTATT 930
Db 558 ThrThr-----ThrThrThrGluAlaThrThrThrThrGluIle 570
QY 931 GTTGCTACAACATAGAACAGTTACAGACAGTACCACTGCTGCTCACTACTTTCACCAAT 990
Db 571 ThrThrThrThrGluGluValThrThrThrThrGluProValThrThrThrThrPro 590
QY 991 CCAAGTGTGTGATAAAACCAAAACAATCGAAATTTTGCACCTATTCACCACTACCATC 1050
Db 591 ThrThrThrSerThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 610
QY 1051 ACAACTTCATATGTTGGTGTGACTACTTCTCTGACTGATAGCTGCACCAATGGTGAA 1110
Db 611 ThrProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 630
QY 1111 ACAGCTACTGTTATTTGTTGATGTGCCATATCATCTACTACCACTGTTACCAGTGAATGG 1170
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Db      631 ThrSerThr-----ThrThrThrThrThrThrThrThrThrThr 642
Qy      1171 ACAGGAACAATCACTACCAACCACTCGTACCAATCCA 1209
        |||  |||  ||| ||| ||| ||| ||| |||
Db      643 ThrAlaThrProThrThrThrThrThrThrMetProPro 655

```

RESULT 13

S48992

Flocculation protein homolog YHR211w - yeast (*Saccharomyces cerevisiae*)

C/Species: *Saccharomyces cerevisiae*

C/Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004

C/Accession: S48992

R/Macri, C.

submitted to the EMBL Data Library, February 1994

A/Description: The sequence of *S. cerevisiae* cosmid 9177.

A/Reference number: S46671

A/Accession: S48992

A/Molecule type: DNA

A/Residues: 1-1075 <NAC>

A/Cross-references: UNIPROT:P38894; EMBL:U00029; NID:G551322; PID:G458919; GSFPDB:GN00008

C/Genetics:

A/Gene: SGD:FLO5; MIPS:YHR211w

A/Cross-references: SGD:S0001254

A/Map position: 8R

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Alignment Scores:
Pred. No.: 0.000198 Length: 1075
Score: 161.50 Matches: 110
Percent Similarity: 33.74% Conservative: 57
Best Local Similarity: 22.22% Mismatches: 209
Query Match: 7.03% Indels: 119
DB: 2 Gaps: 22

US-09-715-876-7 COPY 52 1296 (1-1245) x S48992 (1-1075)

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A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2224
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1428 <KUR>
A;Cross-references: UNIPROT:Q8YRU7; GB:BA000019; PIDN:BAB75045.1; PID:gi7132441; GSPDB:C
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all3346

Alignment Scores:
Pred. No.: 0.000221 Length: 1428
Score: 161.00 Matches: 118
Percent Similarity: 33.40% Conservative: 43
Best Local Similarity: 24.48% Mismatches: 191
Query Match: 7.01% Indels: 130
DB: 2 Gaps: 24

US-09-715-876-7_COPY_52_1296 (1-1245) x AC2224 (1-1428)

QY	34	TCATTAACCTGGTCCATGCTGCTAAT-----TATGCTTTCARAGGGCCAGGATACCCA	87
DB	808	SerValThrGluAspGlyThrProAsnLeuIleTyrThrPheThrArgThrGlySerThr	827
QY	88	ACTTGCATGCTGTTTGGGTGGTCTTAGATGTCACAGTCCCAATCCAGGGGAT---	144
DB	828	ThrAsnAlaLeuThrValAsnTyrSerValAlaGlyThrAlaThrLeuAsnThrAspTyr	847
QY	145	-----ACATTCACATGGAATATGCCA	165
DB	848	AlaGlnThrGlyAlaAlaSerPheThrAlaThrThrGlyThrIleThrPheAlaValGly	867
QY	166	TGTGTGTTTAAATATACCTTACAAACATCTGTTGATTAACTGCCGATGGTGTAA	225
DB	868	AlaSerThrAlaIleLeuThrIleAsnProThrAlaAspThrThrValGluSerAsnGlu	887
QY	226	TATGCTACTGTGCAATTTTATCTGCTGAAGAATTCACAACTTTTCTACATTAACATGT	285
DB	888	ThrValAlaLeuThrLeuAlaSerGlyThrGlyTyrThrValGlyThrThrAlaVal	907
QY	286	ACT-----GTGAACGACGCTTTGAAATCA-----TCC	312
DB	908	ThrGlyThrIleThrAsnAspPheProSerIleThrLeuAlaValSerProAlaSer	927
QY	313	ATTAGGCCATTGGTACAGTT-----	333
DB	928	ValThrGluAspGlyThrProAsnLeuIleTyrThrPheThrArgThrGlySerThrThr	947
QY	334	---ACTTTACCAATTCATTCATCAATGTTGTGGAACAGGTTCA---TCAACTGATTGGAA	387
DB	948	AsnAlaLeuThrIleAsnPheGlyValAlaGlyThrAlaThrLeuAsnThrAspTyrAla	967
QY	388	GATTCT-----AAATGTTTACTGCTGTCACCAATACAGTCACATTTAATGATGGTGT	441
DB	968	GlnSerGlyAlaAlaSerPheThrAlaThrThrGlyThrIleThrPheAlaAlaGlyAla	987
QY	442	AAAGATATCTCAATTGATGTTGAGTTGAAAGTCAACGGTTGATCCAAAGTCATATTGT	501
DB	988	SerThrAlaIleLeu-----ThrIleAsnProThrAla-----	998
QY	502	TATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCAACAATCTTTTGTGSCACCA	561
DB	999	-----AspThrThrValGluSerAsnGluThrValAlaLeuThrLeuAla-----	1013
QY	562	TGTGAAAATGGTTTACATCTCGTACAAATGGGGTCTCCAGTAGTAACGGTACCGTGTCT	621
DB	1014	SerGlyThrGlyTyrThrValGlyThrThr-----ThrAlaValThrGlyThrIleThr	1031
QY	622	ATTGATGCTCAAAATATTCATATTGGTATCAAAAAGGATTAAATGATGGAAATATCCG	681
DB	1032	AsnAsp---AspThrLeuProThrGlyIleThrIleAsnLeuSerGlySerGlnThrIle	1050
QY	682	GTT-----TCATCTGAATCATTTAGTTACACTAAAACTTTGTACATCTAATGGA	729

DB	1051	ValGluGlyAsnSerSerProGlnAsnValThrTyrThrValThrLeuSerGlnAlaSer	1070
QY	730	ATTCCAGATTAAATATCAAAATGTACCTGCTGCTTATCGTCCATTTATTGATGCTTAT	789
DB	1071	SerGlnIle-----lleThrValGlnTyrAla	1079
QY	790	TCGTCTACAGATGTTAACCAATATACCTTATAGCATATATACCAATGATTTATCTGTGCTGGC	849
DB	1080	ThrAlaAsnGly-----ThrAlaThrAlaGlySerAspTyrThrSerThrThr	1095
QY	850	AGTCGCTCTGCAAGTAAACCT-----	870
DB	1096	GlyThrLeuThrPheAsnProGlyGluThrSerIysValIleAsnIleProIleLeuAsn	1115
QY	871	-----TTCACCTTTTAAGATGGACTGGATACATACCAAGTGTGATAAAACCAAAATAGT	903
DB	1116	AspSerValAsnGluAlaAsnGluThrPheThrLeuArgLeuThrSerProThrAsnAla	1135
QY	904	GATGCCGATCTAACGGTATTGTTCATTTGTGTACAACTAGAACAGTTTACAGAC-----	957
DB	1136	ThrLeuGlyThrThrAsnThrVal-----ThrThrThrIleThrAspThrLeu	1151
QY	958	AGTACCACTGCTGCTACTTACATTCATTCACCACTTCCACCATCATCACA---ACTTCATATGTTGGTGTGACT	1074
DB	1152	SerAlaSerValThrThrLeuProThrAsn-----Val	1163
QY	1018	GAATTTTTCACCTATTCACCACTTCCACCATCATCACA---ACTTCATATGTTGGTGTGACT	1074
DB	1164	GluAsnLeuThrLeuThrGlyThrAlaIleAsnGlyThrGlyAsnAlaGly-----	1181
QY	1075	ACTTCCTATCTGACTAAGACTGCACCAATTTGGTGAACACAGCTACTGTTATTGTTGAT---	1131
DB	1182	AsnAsnIleLeuThr-----GlyAsnSerGlyAsnAsnIleLeuSerGly	1196
QY	1132	---GTGCCATATCATCTACCAACCTGTTACCACTGTAAGTGAATGGACAGGAACAATCACTACC	1188
DB	1197	GlyAlaGlyAsnAspThrTyrAlaPheValAlaAlaAlaLeuGlyThrAspThrIle	1216
QY	1189	ACCACAACTCGTACCAATCCCACTGATTCATTAATTCAC-----ACAGTGTGTGTA	1236
DB	1217	ThrGluThrAlaThrGlyIleAspThrIleAspPheAsnGlySerThrAlaThrVal	1236
QY	1237	CAAGTT 1242	
DB	1237	ArgVal 1238	

RESULT 15

T22696
hypothetical protein F55B11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22696
R;Ainscough, R.
A;Reference number: Z19601
A;Submitted to the EMBL Data Library, December 1996
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-851 <WIL>
A;Cross-references: UNIPROT:Q17893; EMBL:Z83318; PIDN:CAB05903.1; GSPDB:GN00022; CESP:
A;Experimental source: clone F55B11
C;Genetics:
A;Gene: CESP:F55B11.3
A;Map position: 4
A;Introns: 49/3, 123/3, 226/1, 282/3, 669/3, 743/3

Alignment Scores:
Pred. No.: 0.00051 Length: 851
Score: 156.00 Matches: 87
Percent Similarity: 31.40% Conservative: 32
Best Local Similarity: 22.96% Mismatches: 170
Query Match: 6.79% Indels: 90


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DB:                2                Gaps:                11
US-09-715-876-7_copy_52_1296 (1-1245) x T22696 (1-851)
QY 124 ACCAGTCCCAATCCAGGGGATACATTCACATTGAATATGCATGTGTGTTAAATATACT 183
DB 330 ThrThrProSerGluLeuSerThrThrThrAlaSerValPro----- 343
QY 184 ACTTCACAAACATCTGTTGATTTAACTGCGCATGGTGTAAATATGCTACTTGTCAATTT 243
DB 344 ThrThrThrThrSerValProThrThrThrThrThrValProThrThrThr----- 360
QY 244 TATTCTGGTGAAGAATTACAACTTTTTCACATTAACATGTAACATGTAAGACGCGTTTG 303
DB 361 -----ThrThrValProThrThrThrThrThrThrValSerThrThr----- 373
QY 304 AAATCATCCATTAAAGCAATTTGGTACAGTTACTTACCAATTCGATTCATTTGGTGA 363
DB 374 -----ThrThrValPro----- 378
QY 364 ACAGTTTCATCAACTGATTTTGAAGATTTCTAAATGTTTTACTGCTGGTACCAATACAGTC 423
DB 379 -----ThrThrThrThrThrThrValProThrThrThrThrThrThrThrThr 396
QY 424 ACATTTAATGATGGTGATAAGATATCTCAATTGATGTTGAGTTTGAAGAGTCAACCGTT 483
DB 397 Thr-----ValProThrThrThrThrVal 405
QY 484 GATCCAAAGTGCAATATTGTATGCTTCAGAGTTATGCCAAGTCTCAATAAGTTCACAACT 543
DB 406 Pro-----ThrThr 408
QY 544 CTTTTTGGGCACCACCAATGGAATGGTTTACACATCTGGTCAATGGGGTTCCTCCAGT 603
DB 409 ThrThrThrThrValProThrThrThrThrThrThrValProThrThrThrThrThr 428
QY 604 AGTAAACGGTGACGTTGCTATTGATTTGCTCAAAATATCATATTTGGTATCACAAAAGGATTA 663
DB 429 ThrThrThrThrValProThrThrThrThrVal----- 440
QY 664 AATGATTGGAAATTATCCGGTTTCATCTGAATCATTTAGTTACATAAACT----- 714
DB 441 -----ProThrThrThrThrThrThrValPro 455
QY 715 TGTACATCTAATGGAATTCAGATTAATAATATCAAAATGTACCTGCTGGTTATCGTCCATTT 774
DB 456 ThrThrThrThrThrThrValSerThrThrThrThrThrThrValProThr----- 470
QY 775 ATTGATGCTTATATTCTGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGAT 834
DB 471 -----ThrThrThrThrThrThrValProThrThrThrThrThrThrThrThr 485
QY 835 TATACCTGCTGGCAGTCGCTCGAAGATAACCTTTTCACTTTAAGATGGACTGGATAC 894
DB 486 ThrThrThrThrValProThrThrThrThrSerValProThrThrThrThrThrThr 505
QY 895 AAGAAATAGTATGCGGATCTAAACGGTATTGCTGTTGCTACAACTAGAAACAGTTTACA 954
DB 506 ThrThrThrThrThrThrValProThrThrThrThrThrThrThrThrThrThrThr 525
QY 955 GACAGTACCACTGCTGCTACTTACCATTCAATCCAACTCACTACATTCATATGTTGGTGTGACT 1014
DB 526 ThrThrThrThrThrThrValProThrThrThrThrThrThrThrThrThrThrThr 545
QY 1015 ATCGAAATTTGCAACCTATTCCCAACCACTACCATTCACAACTTCATATGTTGGTGTGACT 1074
DB 546 ProThrThrThrThrThrThrValProThrThrThrThrThrThrThrThrThrThrThr 565
QY 1075 ACTTCCTATCTGACTAAGACTGACCAATTTGGTGAACAGCT-----ACTGTTATTGTT 1128
DB 566 ValProThrThrThrThrThrThrAlaProThrThrThrThrThrThrThrThrThrThrThr 585
QY 1129 GATGTGCCATATCATATACCACTGTTTACCAGTGAATGGACAGGAACAAATCACTACC 1188
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DB 586 ThrValPro---ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 604
QY 1189 ACCACAACTCGTACCAATCCAACTGATTCAAATTTGACACAGTGGTGGTACAAAGTTCCA 1245
DB 605 ThrThrThrThrValProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 623
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Search completed: September 8, 2005, 17:51:13
Job time : 81 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 8, 2005, 17:10:51 : Search time 200 Seconds

(without alignments)
4815.167 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296

Perfect score: 2297

Sequence: 1 aagacaatcactgtgtttt.....cagtggtggtacaagtcca 1245

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2_1/USPTO_spool_p/US0715876/runat_08092005_172226_18474/app_query.fasta_1.1415
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNIT5=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0715876 @CGN_1_1_224 @runat_08092005_172226_18474 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2174	94.6	1260	7 ABW01168	Abw01168 Candida a
2	1885	82.1	1119	7 ABW01170	Abw01170 Candida a
3	1865	81.2	1270	7 ABW01172	Abw01172 Candida a
4	1832	79.8	1047	7 ABW01175	Abw01175 Candida a
5	1769.5	77.0	468	7 ABW01169	Abw01169 Candida a
6	1596	69.5	469	7 ABW01171	Abw01171 Candida a
7	1544.5	67.2	468	7 ABW01176	Abw01176 Candida a
8	1500	65.3	1443	7 ABW01173	Abw01173 Candida a
9	961.5	41.9	2297	7 ABW01174	Abw01174 Candida a
10	308.5	13.4	650	2 AAR47575	Aar47575 Alpha-agg

ALIGNMENTS

RESULT 1

ABW01168
ID ABW01168 standard; protein; 1260 AA.

XX AC ABW01168;

XX DT 15-JAN-2004 (first entry)

XX DE Candida albicans agglutinin-like sequence (ALS) 1 protein.

XX KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX KW candidiasis; vaccine; fungicide.

XX OS Candida albicans.

XX PN US2003124134-A1.

XX PD 03-JUL-2003.

XX PF 13-SEP-2002; 2002US-00245802.

XX PR 19-NOV-1999; 99US-0166663P.

XX PR 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX N-P8DB; AD62305.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of

PT the organism.
XX Disclosure; Page 14-17; 65pp; English.
PS
XX The present invention relates to a monoclonal antibody against an agglutinin-like sequence (ALS)1 protein that specifically binds an epitope in an N-terminal domain and which inhibits adherence of Candida albicans to endothelial cells. The invention is useful as vaccines for treating and preventing disseminated candidiasis and for generating an immune response capable of blocking adherence of the organism. The invention is also useful in gene therapy. The present sequence is Candida albicans agglutinin-like sequence (ALS) protein
XX
SQ Sequence 1260 AA;

Alignment Scores:
Pred. No.: 6,18-199 Length: 1260
Score: 2174.00 Matches: 413
Percent Similarity: 99.52% Conservative: 2
Best Local Similarity: 99.52% Mismatches: 0
Query Match: 94.65% Indels: 0
DB: 7 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x ABW01168 (1-1260)

QY 1 AAGCAATCACTGGTGTGTTTGTAGTATTTAAATTCATTAACTTGGTCCAATGCTGCTAAT 60
DB 18 LysThrIleThrGlyValPheAspSerPheAsnSerLeuThrTrpSerAsnAlaAsn 37
QY 61 TATGCTTTCAAGGCCAGGATCCCAACTTGGAAATGCTGTTTGGGTTCCTTAGAT 120
DB 38 TyrAlaPheLysGlyProGlyTyrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57
QY 121 GGTACAGTGCATCCAGGGATACATTACATTGAATATGCCATGCTGTTTAATAT 180
DB 58 GlyThrSerAlaAsnProGlyAspThrPheThrLeuAsnMetProCysValPheLysTyr 77
QY 181 ACTACTTCAACAAATCTGTTGATTAACTGCCATGGTGTAAATATGCTACTTGTCAA 240
DB 78 ThrThrSerGlnThrSerValAspLeuThrAlaAspGlyValLysTyrAlaThrCysGln 97
QY 241 TTTTATTCTGGTGAAGAAATTCACAACTTTTCTACATTAACATGCTACTGACGAGCT 300
DB 98 PheTyrSerGlyGluPheThrThrPheSerThrLeuThrCysThrValAsnAspAla 117
QY 301 TTGAATCATCCATTAGGCATTTGGTACAGTACTTTTACCAATTCATTCATTCATTCGT 360
DB 118 LeuLysSerSerIleLysAlaPheGlyThrValThrLeuProIleAlaPheAsnValGly 137
QY 361 GGAACAGGTTTCATCAACTGATTTGGAAGATTCCTAAATGTTTACTGCTGGTACCAATACA 420
DB 138 GlyThrGlySerSerThrAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
QY 421 GTCATATTAAATGATGATGAATAAGATATCTCAATTCATTCATTCATTCATTCATTCATTC 480
DB 158 ValThrPheAsnAspGlyAspLysAspIleSerIleAspValGluPheGluLysSerThr 177
QY 481 GTTCATCCAGTGCATATTTGATGCTTCCAGATGTTATGCCAGTCTCAATATAGGTCCACA 540
DB 178 ValAspProSerAlaTyrLeuTyrAlaSerArgValMetProSerLeuAsnLysValThr 197
QY 541 ACTCTTTTGGGCCACCAATGTAAGAAATGGTTACATCTGCTACATCTGCTACATGGGGTTCTCC 600
DB 198 ThrLeuPheValAlaProGlnCysGluAsnGlyTyrThrSerGlyThrMetGlyPheSer 217
QY 601 AGTAGTAACGGTGCATGCTTATTCATTCCTCAATATTCATATTCATATTCATATTCATATTC 660
DB 218 SerSerAsnGlyAspValAlaIleAspCysSerAsnIleHisIleGlyIleThrLysGly 237
QY 661 TTAATATGATTCGAATATCCGGTTTCATCTCAATCATTCATCTCAATCATTCATCTCAATCAT 720
DB 238 LeuAsnAspTrpAsnTyrProValSerSerGluSerPheSerTyrThrLysThrCysThr 257

QY 721 TCTAATGGAATTCAGATTAAATATCAAAATGATACCTGCTGGTATTCGTCCATTATTATGAT 780
DB 258 SerAsnGlyIleGlnIleLysTyrGlnAsnValProAlaGlyTyrArgProPheIleAsp 277
QY 781 GCTTATATTTCTGCTACAGATCTTAACCAATATCTTTAGCATATATACCAATGATATATCT 840
DB 278 AlaTyrIleSerAlaThrAspValAsnGlnTyrThrLeuAlaTyrThrAsnAspTyrThr 297
QY 841 TGTGCTGGCAGTCGCTGCAAAAGTAAACCTTTTCACTTTAAGATGGAAGTACGATACAGAAT 900
DB 298 CysAlaGlySerArgSerGlnSerLysProPheThrLeuArgTyrThrGlyTyrLysAsn 317
QY 901 AGTGATGCCGATCTAAACGGTATTCATTTGCTGCTACCACTAGAACAGTTACAGACAGT 960
DB 318 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 337
QY 961 ACCACTGCTGCTCACTACTTTTACCATTCATCCAAAGTGTGTAAACCAACCAATCGAA 1020
DB 338 ThrThrAlaValThrThrLeuProPheAsnProSerValAspLysThrLysThrIleGlu 357
QY 1021 ATTTTCAACCTATTCCAAACCACTACCATCACAACCTTCATATGTTGGTGTGACTACTTCC 1080
DB 358 IleLeuGlnProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 377
QY 1081 TATCTGACTAAGACTGCAACAAATGCTGAAACAGCTACTGTTATTTGTTGATGTCATAT 1140
DB 378 TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspValProTyr 397
QY 1141 CATACTACCACTGTTTACCAGTGAATGAGCAGGAGCAACATCATTACCACTCACTCGT 1200
DB 398 HisThrThrThrThrValThrSerGluTrpThrGlyThrIleThrThrThrThrThrArg 417
QY 1201 ACCAACTCAACTGATTCAATTCACACAGTGGTGTGCAAGTTCCA 1245
DB 418 ThrAsnProThrAspSerIleAspThrValValValGlnValPro 432
RESULT 2
ABW01170
ID ABW01170 standard; protein; 1119 AA.
XX
XX ABW01170;
AC
XX
DT 15-JAN-2004 (first entry)
XX
DE Candida albicans agglutinin-like sequence (ALS) 3 protein.
XX
KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide.
XX
OS Candida albicans.
XX
XX US2003124134-A1.
XX
XX 03-JUL-2003.
XX
XX 13-SEP-2002; 2002US-00245802.
XX
XX 19-NOV-1999; 99US-0166663P.
XX
XX 18-NOV-2000; 2000US-00715876.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Edwards JE, Fuller SG, Sheppard DC, Ibrahim A, Fu Y;
XX
XX WPI; 2003-810971/76.
XX
XX N-PSDB; AAD62307.
XX
XX New monoclonal antibody against Candida albicans agglutinin-like sequence
XX 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
XX candidiasis, or to generate an immune response that blocks adherence of
XX the organism.
XX
XX Disclosure; Page 21-23; 65pp; English.
PS

XX The present invention relates to a monoclonal antibody against an
 CC agglutinin-like sequence (ALS)1 protein that specifically binds an
 CC epitope in an N-terminal domain and which inhibits adherence of Candida
 CC albicans to endothelial cells. The invention is useful as vaccines for
 CC treating and preventing disseminated candidiasis and for generating an
 CC immune response capable of blocking adherence of the organism. The
 CC invention is also useful in gene therapy. The present sequence is Candida
 CC albicans agglutinin-like sequence (ALS) protein
 XX
 SQ Sequence 1119 AA;

Alignment Scores:
 Pred. No.: 2,98e-171 Length: 1119
 Score: 1885.00 Matches: 352
 Percent Similarity: 92.05% Conservative: 30
 Best Local Similarity: 84.82% Mismatches: 33
 Query Match: 82.06% Indels: 0
 DB: 7 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x ABW01170 (1-1119)

QY 1 AAGCAATCACTGGTGTGTTTTCATAGTTTAAATCAATTAATGTTTCAATGCTGCTAAAT 60
 DB 18 LysThrIleThrGlyValPheAsnSerPheAsnSerLeuThrTrpSerAsnAlaAlaThr 37
 QY 61 TATGCTTTCAAGGCCAGGATACCAACTTGGATGCTGTTTGGGTGCTCTAGAT 120
 DB 38 TyrAsnTyrLysGlyProGlyThrProThrTrpAsnAlaValLeuGlyTrpSerLeuAsp 57
 QY 121 GGTACCACTGCAATCCAGGGGATACATTCATTAATGATATGCAATGCTGTTTAAATAT 180
 DB 58 GlyThrSerAlaSerProGlyAspThrPheThrLeuAsnMetProCysValPheLysPhe 77
 QY 181 ACTACTTCACAAACATCTGTTGAATTAATCTGCCGATGGTGTAAATATGCTACTTGTCAA 240
 DB 78 ThrThrSerGlnThrSerValAspLeuThrAlaHisGlyValLysTyrAlaThrCysGln 97
 QY 241 TTTTATCTGTTGAAGAATTCACAACTTTTCTACATTAACATGCTACTGTGACGACCT 300
 DB 98 PheGlnAlaGlyGluGluPheMetThrPheSerThrLeuThrCysThrValSerAsnThr 117
 QY 301 TTGAATCATCATTAAGGCATTTGTTGATGCTGTTTACCAATGCAATTCATGTTTGGT 360
 DB 118 LeuThrProSerIleLysAlaLeuGlyThrValThrLeuProLeuAlaPheAsnValGly 137
 QY 361 GGAACAGGTTTCATCAACTGATTTGGAAGATTCATAATGTTTACTGCTGGTACCAATACA 420
 DB 138 GlyThrGlySerSerValAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
 QY 421 GTCAATTTAATGATGGTGATTAAGATATCTCAATTTGATGTTGAGTTTGAAAGTCAACC 480
 DB 158 ValThrPheAsnAspGlyGlyLysLysIleSerIleAsnValAspPheGluArgSerAsn 177
 QY 481 GTTGTATCCAAGTGCATATTTGATGCTTCCAGTTTATGCCAAGTCTCAATTAAGGTACAC 540
 DB 178 ValAspProLysGlyTyrLeuThrAspSerArgValIleProSerLeuAsnLysValSer 197
 QY 541 ACTCTTTTGTGGCCACCAATGTGAAATGTTTACACATCTGTGTACCAATGGGGTCTCC 600
 DB 198 ThrLeuPheValAlaProGlnCysAlaAsnGlyTyrThrSerGlyThrMetGlyPheAla 217
 QY 601 AGTAGTAAGGTGAGCTGCTATTGATGCTCAATATTCATATTCATATTCATATTCATATTC 660
 DB 218 AsnThrTyrGlyAspValGlnIleAspCysSerAsnIleHisValGlyIleThrLysGly 237
 QY 661 TTAATGATGGAATATCCGTTTCACTGATCATTTAGTTTACACTTAAACTTGTACA 720
 DB 238 LeuAsnAspTrpAsnTyrProValSerSerGluSerPheSerThrLysThrCysSer 257
 QY 721 TCTAATGGAATTCAGATTAATATCAAAATGTACCTGCTGGTTATCGTCAATTTATGAT 780
 DB 258 SerAsnGlyIlePheIleThrTyrLysAsnValProAlaGlyTyrArgProPheValAsp 777

QY 781 GCTTATATTTCTGTACAGATGTTAAACCAATATATCTTTAGCATATATACCAATGATTACT 840
 DB 278 AlaTyrIleSerAlaThrAspValAsnSerTyrThrLeuSerTyrAlaAsnGlyTyrThr 297
 QY 841 TGTGCTGGCAGTCTGCTGCAAGATAAACCTTTTACATTTAAGTAGGACTGATACACAAT 900
 DB 298 CysAlaGlyGlyTyrTrpGlnArgAlaProPheThrLeuArgTrpThrGlyTyrArgAsn 317
 QY 901 AGTGATGCCGATCTAACGGTATTGTCATTTGTTGCTCAACTAGAACAGTTTACAGACAGT 960
 DB 318 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 337
 QY 961 ACCACTGCTGCTACTTCTTACCATTCATCCAAAGTGTTCATATAAAACCAAAACCAATCGAA 1020
 DB 338 ThrThrAlaValThrThrLeuProPheAspProAsnArgAspLysThrLysThrIleGlu 357
 QY 1021 ATTTTGGAACTATTCCAACTACCATCACAACCTTCATATGTTGGTGTGACTACTTCC 1080
 DB 358 IleLeuLysProIleProThrThrIleThrThrSerTyrValGlyValThrThrSer 377
 QY 1081 TATCTGACTAAGACTGCACCAATTTGGTGAACAGTACTGTTATTGTTGATGTCCTAT 1140
 DB 378 TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspIleProTyr 397
 QY 1141 CATACTACCACTGTTTACAGTGAATGAGAGAGAAACAATCACTACCACCACTCGT 1200
 DB 398 HisThrThrThrValThrSerLysThrLysThrGlyThrIleThrSerThrThrHis 417
 QY 1201 ACCAATCCAATCAATTCATGACACAGTGGTGTGACAGTTCCA 1245
 DB 418 ThrAsnProThrAspSerIleAspThrValIleValGlnValPro 432

RESULT 3

ABW01172
 ID ABW01172 standard; protein; 1270 AA.

XX AC ABW01172;

XX DT 15-JAN-2004 (first entry)

XX DE Candida albicans agglutinin-like sequence (ALS) 5 protein.

XX XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
 candidiasis; vaccine; fungicide.

XX OS Candida albicans.

XX XX US2003124134-A1.

XX PD 03-JUL-2003.

XX PF 13-SEP-2002; 2002US-00245802.

XX PR 19-NOV-1999; 99US-0166663P.

XX PR 18-NOV-2000; 2000US-00715876.

XX XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX XX N-PSDB; AAD62309.

XX XX WPI; 2003-810971/76.

XX XX New monoclonal antibody against Candida albicans agglutinin-like sequence
 PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
 PT candidiasis, or to generate an immune response that blocks adherence of
 PT the organism.

XX PS Disclosure; Page 27-31; 65pp; English.

XX XX The present invention relates to a monoclonal antibody against an
 CC agglutinin-like sequence (ALS)1 protein that specifically binds an

CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) protein
XX
SQ Sequence 1047 AA;

Alignment Scores:
Pred. No.: 3,49e-166 Length: 1047
Score: 1832.00 Matches: 346
Percent Similarity: 92.05% Conservative: 36
Best Local Similarity: 83.37% Mismatches: 33
Query Match: 79.76% Indels: 0
DB: 7 Gaps: 0

US-09-715-876-7_COPY_52_1296 (1-1245) x ABW01169 (1-1047)

Qy 1 AAGCAATCACTGCTGTTTGTAGTATTAATTAATCACTGCTGCTCAATGCTGCTAAT 60
Db 18 LysThrIleThrGlyValPheAsnSerPheAsnSerLeuThrThrSerAsnAlaAlaThr 37
Qy 61 TATGCTTTCAAGGCCAGGATCCCAACTTGGATGCTGTTTGGTGGTCTCTAGAT 120
Db 38 TyrHisTyrLysGlyProGlyThrProThrThrAsnAlaValLeuGlyTyrSerLeuAsp 57
Qy 121 GGTACCACTGCAATCCAGGGGATACATTCACATTTGAATATGCTGTTTAAATAT 180
Db 58 GlyThrSerAlaSerProGlyAspThrPheThrLeuAsnMetProCysValPheLysPhe 77
Qy 181 ACTACTTCACAAATCTGTTGATTTAACTCCGATGCTGTTAAATATGCTACTTGTCAA 240
Db 78 ThrThrSerGlnThrSerValAspLeuThrAlaHisGlyValLysTyrAlaThrCysGln 97
Qy 241 TTTTATCTGCTGGAAGATTCACAACTTTTCTACATTAACATGCTACTGCTGGAAGCGCT 300
Db 98 PheGlnAlaGlyGluGluPheMetThrPheSerThrLeuThrCysThrValSerAsnThr 117
Qy 301 TTGAATCATCATTAAGCATTTGGTACAGTACTTTTACCAATGCTGCTCAATGCTGCT 360
Db 118 LeuThrProSerIleLysAlaLeuGlyThrValThrLeuProLeuAlaPheAsnValGly 137
Qy 361 GGAACAGGTTTCATCAATGATTTGAAGATTTCTAAATGTTTACTGCTGCTGCTCAATACA 420
Db 138 GlyThrGlySerSerValAspLeuGluAspSerLysCysPheThrAlaGlyThrAsnThr 157
Qy 421 GTCATTTATGATGCTGATTAAGATATCTCAATTTGATGCTGCTGCTGCTGCTGCTGCT 480
Db 158 ValThrPheAsnAspGlyGlyLysLysIleSerIleAsnValAspPheGluArgSerAsn 177
Qy 481 GTTGATCCAAGTGCATATTTGATGCTTCCAGATTTATGCCAAGTCTCAATAGCTCACA 540
Db 178 ValAspProLysGlyTyrLeuThrAspSerArgValIleProSerLeuAsnLysValSer 197
Qy 541 ACTCTTTTGTGGCCACCAATGTGAAATGTTTACACATCTGCTGCTGCTGCTGCTGCTGCT 600
Db 198 ThrLeuPheValAlaProGlnCysAlaAsnGlyTyrThrSerGlyThrMetGlyPheAla 217
Qy 601 AGTAGTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 218 AsnThrTyrGlyAspValGlnIleAspCysSerAsnIleHisValGlyIleThrLysGly 237
Qy 661 TTAATGATTTGGAATTTATCCGTTTTCATCTGATTCATTTAGTTTACACTAAAATGTTACA 720
Db 238 LeuAsnAspTyrAsnTyrProValSerSerGluSerPheSerTyrThrLysThrCysSer 257
Qy 721 TCTAATGGAATTCAGATTAATATCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 258 SerAsnGlyIlePheIleThrTyrLysAsnValProAlaGlyTyrArgProPheValAsp 277
Qy 781 GCTTATATTTGCTACAGATTTAAACCAATATATCTTTAGCATATACCAATGATTTACT 840
Db 278 AlatyrlleSerAlaThrAspValAsnSerTyrThrLeuSerTyrAlaAsnGlyTyrThr 297
Qy 841 TGTGCTGGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

Db 298 CysAlaGlyGlyTyrTyrGlnArgAlaProPheThrLeuArgTyrThrGlyTyrArgAsn 317
Qy 901 AGTGATGCGGATCTAAACGGTATTGTCATTGTTGCTACCACTAGAACAGTTACAGACAGT 960
Db 318 SerAspAlaGlySerAsnGlyIleValIleValAlaThrThrArgThrValThrAspSer 337
Qy 961 ACCACTGCTGCTACTACTTTTACCAATCAATCCAAAGTGTGATATAAACCACCAATCGAA 1020
Db 338 ThrThrAlaValThrThrLeuProPheAspProAsnArgAspLysThrLysThrIleGlu 357
Qy 1021 ATTTGCAACCTATTCCACCACTTACCATCACAATTCATATGTTGGTGTGCTACTTCC 1080
Db 358 IleLeuLysProIleProThrThrThrIleThrThrSerTyrValGlyValThrThrSer 377
Qy 1081 TATCTGCTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATTTGTTGATGTGCCATAT 1140
Db 378 TyrSerThrLysThrAlaProIleGlyGluThrAlaThrValIleValAspIleProTyr 397
Qy 1141 CATACTACCACTGTTTACCACTGATGAGAGGAACTCAATCACTACCAACCACTCGT 1200
Db 398 HisThrThrThrThrValThrSerLysTyrThrGlyThrIleThrSerThrThrHis 417
Qy 1201 ACCAATCCAACTGATTCATTTGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1245
Db 418 ThrAsnProThrAspSerIleAspThrValIleValGlnValPro 432

RESULT 5

ABW01169
ID ABW01169 standard; protein; 468 AA.

XX AC ABW01169;

XX DT 15-JAN-2004 (first entry)

XX DE Candida albicans agglutinin-like sequence (ALS) 2 protein.

XX KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
XX KM candidiasis; vaccine; fungicide.

XX OS Candida albicans.

XX FH Key Location/Qualifiers

FT Misc-difference 41

FT /note= "Encoded by AAC"

XX FN US2003124134-A1.

XX PD 03-JUL-2003.

XX PP 13-SEP-2002; 2002US-00245802.

XX PR 19-NOV-1999; 99US-0166663P.

XX PR 18-NOV-2000; 2000US-00715876.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Edwards JB, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX DR WPI; 2003-810971/76.

XX DR N-PSDB; AAD62306.

XX PT New monoclonal antibody against Candida albicans agglutinin-like sequence
XX CC 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
XX PT candidiasis, or to generate an immune response that blocks adherence of
XX PT the organism.

XX PS Disclosure; Page 18-19; 65pp; English.

XX CC The present invention relates to a monoclonal antibody against an
XX CC agglutinin-like sequence (ALS)1 protein that specifically binds an
XX CC epitope in an N-terminal domain and which inhibits adherence of Candida
XX CC albicans to endothelial cells. The invention is useful as vaccines for

Alignment Scores:			
Pred. No.:	8.91e-139	Length:	468
Score:	1544.50	Matches:	291
Percent Similarity:	83.13%	Conservative:	54
Best Local Similarity:	70.12%	Mismatches:	69
Query Match:	67.24%	Indels:	1
DB:	7	Gaps:	1
US-09-715-876-7_COPY_52_1296 (1-1245) x ABW01176 (1-468)			
QY	1	AAGACAATCACTGGTGTGTTTTGATAGTGTAAATTCATTAACTTGGTCCAAATGCTGCTTAAT	60
DB	18	LysThrIleThrGlyValPheAsnSerPheAspSerLeuThrThrArgSerValGlu	37
QY	61	TATGCTTTCAAGGCCAGGATACCCAACTTGGATGCTGTTGGGTGGTCTTACAT	120
DB	38	TyrAlaTyrLysGlyProGluThrProThrTyrAsnAlaValLeuGlyTyrSerLeuAsn	57
QY	121	GGTACCAGTGCCAATCCAGGGGATACATTTCATTTGAATATGCCATGTGTGTTTAAATAT	180
DB	58	SerThrThrAlaAspProGlyAspThrPheThrLeuIleLeuProCysValPheLysPhe	77
QY	181	ACTACTTCACAAAACATCTGTTCATTTAACTGCGCATGGTGTAAATATGCTACTTGTC	240
DB	78	IleThrThrGlnThrSerValAspLeuThrAlaAspGlyValSerTyrAlaThrCysAsp	97
QY	241	TTTATTCTGTGTGAAGAAATTCACAACTTTTCTACATAACATGACTGTGTGAACACGCT	300
DB	98	PheAsnAlaGlyGluGluPheThrThrPheSerSerLeuSerCysThrValAsnSerVal	117
QY	301	TTGAAATCATCCATTAAGGCATTTGGTACAGTACTTTTACCAATGTCATTCATCTGCT	360
DB	118	SerValSerTyrAlaArgValSerGlyThrValLysLeuProlIleThrPheAsnValGly	137
QY	361	GGAAACAGCTTCATCAACTGATTTTGGGAAGATTCCTAAATGTTTACTGCTGGTACCAAT	420
DB	138	GlyThrGlySerSerValAspLeuAlaAspSerLysCysPheThrAlaGlyLysAsnThr	157
QY	421	GTCACATTTAATGATGTGTGATAAGATATCTCAATGTGATGTGAGTTTGAAAGTCAACC	480
DB	158	ValThrPheMetAspGlyAspThrLysIleSerThrThrValLysPheAspAlaSerPro	177
QY	481	GTTGATCCAGTGCATATTTGTATGCTTCCAGAGTTATGCCAGTCTCAATTAAGGTCA	540
DB	178	ValSerProSerGlyTyrIleThrSerSerArgIleIleProSerLeuAsnLysLeuSer	197
QY	541	ACTCTTTTGTGGCACCAATGTGAAAATGGTTACACATCTGGTACAAATGGGGTTCCTC	600
DB	198	SerLeuPheValValProGlnCysGluAsnGlyTyrThrSerGlyIleMetGlyPheVal	217
QY	601	AGTAGTAACGGTGACGTGCTTATTCATTTGCTCCAAATATTCATTTGGTATCACAAAG	660
DB	218	AlaSerAsnGly--AlaThrIleAspCysSerAsnValAsnIleGlyIleSerLysGly	236
QY	661	TTAAATGATCGAATTATCCGGTTTCATCTGAATCATTTAGTTACACTAAAACTTGTACA	720
DB	237	LeuAsnAspTyrAsnProValSerSerGluSerPheSerTyrThrLysThrCysThr	256
QY	721	TCTAATGGAATTCAGATTAAATATCAAAATGTACCTGCTGGTTATCGTCCATTTATTTAT	780
DB	257	SerThrSerIleThrValGluPheGlnAsnValProAlaGlyTyrArgProPheValAsp	276
QY	781	GCTTATATTTCTGCTACAGATGTTAACCAATATATCTTTAGCATATATACCAATGATT	840
DB	277	AlaTyrIleSerAlaGluAsnIleAspLysTyrThrLeuThrThrAlaAsnGluTyrThr	296
QY	841	TGTGCTGGCAGTCGCTGCAAGATAAACCTTTTCACTTTTAAGATGGACTGGATACAGA	900
DB	297	CysGluAsnGlyAsnThrValValAspProPheThrLeuThrTyrTyrGlyTyrLysAsn	316
QY	901	AGTGAATCGCGGATCTAAACGGTATTTGTCATTTGTTGTCTACAACTAGAACAGTTT	960

SQ Sequence 1443 AA;

Alignment Scores:

Pred. No.: 2,78e-134 Length: 1443
 Score: 1500.00 Matches: 281
 Percent Similarity: 81.53% Conservative: 59
 Best Local Similarity: 67.39% Mismatches: 75
 Query Match: 65.30% Indels: 2
 DB: 7 Gaps: 1

US-09-715-876-7_COPY_52_1296 (1-1245) x ABW01173 (1-1443)

QY 1 AAGCAATCACTGCTGTTTGTAGTATTAATTAATCAATGCTGCTCAATGCTGCTAAT 60
 DB 19 LysThrIleSerGlyValPheThrSerPheAsnSerLeuThrThrThrAsnThrGlyAsn 38
 QY 61 TATGCTTTCAAAGCCGAGGATACCAACTTGGAAATGCTGTTTGGGTGGTCTTATGAT 120
 DB 39 TyrProTyrGlyGlyProGlyTyrProThrTyrThrAlaValLeuGlyTyrSerLeuAsp 58
 QY 121 GGTACCAAGTCCCAATCCAGGGATACATTCATTCATGATATGCCATGCTGTTTAAATAT 180
 DB 59 GlyThrLeuAlaSerProGlyAspThrPheThrLeuValMetProCysValPheLysPhe 78
 QY 181 ACTACTTCACAAACATCTGTTGATTAACTCCGATGGTGTAAATATGCTACTTGTCAA 240
 DB 79 IleThrThrGlnThrSerValAspLeuThrAlaAsnGlyValLysTyrAlaThrCysThr 98
 QY 241 TTTTATCTGCTGAAGATACCAACTTTTCTACATTAACATGATGCTGTAACGAGCT 300
 DB 99 PheHisAlaGlyGluAspPheThrThrPheSerSerMetSerCysValValAsnAsnGly 118
 QY 301 TTGAATCATCATTAAGGCATTTGGTACAGTACTTACCAATTCATTCATTCATTCAT 360
 DB 119 LeuSerSerAsnIleArgAlaPheGlyThrValArgLeuProIleSerPheAsnValGly 138
 QY 361 GGACAGGTTTCATCACTGATTTGGAAGATCTAAATGTTTACTGCTGGTACCAATACA 420
 DB 139 GlyThrGlySerSerValAsnIleGlnAspSerLysCysPheThrAlaGlyThrAsnThr 158
 QY 421 GTCATATTATATGATGGTGAATAAGATATCTCAATTTGATGTTGAGTTTGAAGTCAAC 480
 DB 159 ValThrPheThrAspGlyAspHisLysIleSerThrThrValAsnPheProLysThrPro 178
 QY 481 GTTGATCCAGTGCAATATTTGATGCTCCAGAGTATGCCAGTCTCAATAAGGTACA 540
 DB 179 GlnSerSerSerSerSerValTyrPheAlaArgValIleProSerLeuAspLysLeuSer 198
 QY 541 ACTCTTTTGGGACCAACAATGTGAAATGTTTACATCTGTTACATCTGGTACCAATGGGTTCTCC 600
 DB 199 SerLeuValValAlaSerGlnCysThrAlaGlyTyrAlaSerGlyValLeuGlyPheSer 218
 QY 601 AGTAGTAACGGTGAAGTCTTATGATGCTCAAAATATTCATATTTGGTATCACAAAAGGA 660
 DB 219 AlaThrLysAspAspValThrIleAspCysSerThrIleHisValGlyIleThrAsnGly 238
 QY 661 TTAATGATGGAATATCCGGTTTCATCTGATCATTTAGTACACTTAAACTGTGTACA 720
 DB 239 LeuAsnSerTyrAsnMetProValSerSerGluSerPheSerTyrThrLysThrCysThr 258
 QY 721 TCTAATGGAATTCAGATTAATATCAAAATGATCTGCTGTTATGCTGCTCAATTTATTCAT 780
 DB 259 ProAsnSerPheIleIleThrTyrGluAsnValProAlaGlyTyrArgProPheIleAsp 278
 QY 781 GCTTATATTTCTGCTACAGATGTTTACCAATATTAATTAATTAATTAATTAATTAAT 834
 DB 279 SerTyrValLysLysSerAlaThrAlaThrAsnGlyPheAsnLeuAsnTyrThrAsnIle 298
 QY 835 TATATCTTGGTGGCAGTCTGTCGAAAGTAAACCTTTCATCTTTAAGATGGCTGGATAC 894
 DB 299 TyrAsnCysMetAspGlyLysLysGlyAsnAspProLeuIleTyrPheTyrThrSerTyr 318
 QY 895 AAGATAGTGTGTCGGGATCTTAACGGTATTGTCATTGTTGCTACCAACTAGAACAGTTACA 954

DB 319 ThrAsnSerAspAlaGlySerAsnGlyAlaAlaValValValThrThrArgThrValThr 338
 QY 955 GACAGTACCACTGCTGCTACTTACCAATTCATCAATCAATCAATCAATCAATCAATCA 1014
 DB 339 AspSerThrThrAlaIleThrThrLeuProPheAspProThrValAspLysThrLysThr 358
 QY 1015 ATCGAAATTTTGCACACCTATTCCACACCATCAATCAATCAATCAATCAATCAATCA 1074
 DB 359 IleGluValIleGluProIleProThrThrThrIleThrThrSerTyrValGlyIleSer 378
 QY 1075 ACTTCTATCTGACTAAGACTGACCAATTTGGTGAACACAGCTACTGTTATTTGATGTG 1134
 DB 379 ThrSerLeuSerThrLysThrAlaThrIleGlyGlyThrAlaThrValValAspVal 398
 QY 1135 CCATATCATACTACCACTGTTTACCAGTGAATGGACAGCAACCAATCACTACCAACACA 1194
 DB 399 ProTyrHisThrThrThrThrIleThrSerIleTyrThrGlySerAlaThrThrSerSer 418
 QY 1195 ACTGCTACCAATCCAACTGATTCATTCATTCATTCATTCATTCATTCATTCATTC 1245
 DB 419 ThrTyrThrAsnProThrAspSerIleAspThrValValGlnValPro 435
 RESULT 9
 ID ABW01174 standard; protein; 2297 AA.
 AC ABW01174;
 XX 15-JAN-2004 (first entry)
 XX Candida albicans agglutinin-like sequence (ALS) 7 protein.
 XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
 XX candidiasis; vaccine; fungicide.
 XX Candida albicans.
 XX US2003124134-A1.
 XX 03-JUL-2003.
 XX 13-SEP-2002; 2002US-00245802.
 XX 19-NOV-1999; 99US-0166663P.
 XX 18-NOV-2000; 2000US-00715876.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Edwards JE, Fuller SG, Sheppard DC, Ibrahim A, Fu Y;
 WPI; 2003-810971/76.
 XX N-PSDB; AAD62311.
 XX New monoclonal antibody against Candida albicans agglutinin-like sequence
 PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
 PT candidiasis, or to generate an immune response that blocks adherence of
 PT the organism.
 XX Disclosure; Page 40-45; 65pp; English.
 XX The present invention relates to a monoclonal antibody against an
 CC agglutinin-like sequence (ALS)1 protein that specifically binds an
 CC epitope in an N-terminal domain and which inhibits adherence of Candida
 CC albicans to endothelial cells. The invention is useful as vaccines for
 CC treating and preventing disseminated candidiasis and for generating an
 CC immune response capable of blocking adherence of the organism. The
 CC invention is also useful in gene therapy. The present sequence is Candida
 CC albicans agglutinin-like sequence (ALS) protein
 XX Sequence 2297 AA;
 SQ Alignment Scores:

PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 22177; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 650 AA;

Alignment Scores:

Pred. No.: 3,46e-20 Length: 650
Score: 308.50 Matches: 116
Percent Similarity: 43.33% Conservative: 79
Best Local Similarity: 25.78% Mismatches: 190
Query Match: 13.43% Indels: 65
Db: 8 Gaps: 20

US-09-715-876-7_COPY_52_1296 (1-1245) x ADS43747 (1-650)

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QY 25 AGTTTAAATCATTAACCTGGTCCAAAT-----GCTGCTAATTATGCT 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 AnleleAsnAspIleThrPheSerAsnLeuGluIleThrProLeuThrAlaAsn----- 38

QY 67 TTCAAAGGCCAGGATACCCAACTTGGAACTGCTTTTGGGTGGTCTCTTA---GATGGT 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 39 ---LysGlnProAsp--GlnGlyTrpThrAlaThrPheAspPheSerIleAlaAspAla 56

QY 124 ACCAGTGCCATCCAGGGATACATTCATTTGAATGATGCGATGCTGTTTAA----- 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 57 SerSerIleArgGluGlyAspGluPheThrLeuSerMetProHisValTyrArgIleLys 76

QY 178 ---TATACTACTTCACAACTCTGTTGATTAACTGCGATGCTGTTAAATATGCTACT 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 LeuLeuAsnSerSerGlnThrAlaThrIleSerLeuAlaAspGlyThrGluAlaPheLys 96

QY 235 TGTCATTTTATCTCGTGAA-----GAATTCACAACTTTTCTTACATTA 279
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 97 Cys---TyrValSerGlnAlaAlaTyrLeuTyrGluAsnThrThrPhe----- 112

QY 280 ACATGTACTGTGAACGAGCTTTGAAATCATCCATTAAAGGCATTTGGTACAGTTACTT 339
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 ThrCysThrAlaGlnAsnAspLeuSerSerTyrAsnThrIleAspGlySerIleThrPhe 132

QY 340 CCAATTGCTATTCATTTGGTGGACAGGTTTCATCACTGATTTGGAGATTTCTAAATGT 399
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 SerLeuAsnPheSerAspGlyGlySerSerTyrGluTyrGluLeuGluAsnAlaLysPhe 152

QY 400 TTTACTGCTGGTACCAATPACATGTCACATTTAATGATGGTGATATAAGATATCTCAATGAT 459
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 153 PheLysSerGlyProMetLeuValLysLeuGlyAsnGlnMetSerAspVal----- 169
QY 460 GTTGAGTTGAAAGTCAACCGTGTGATCCAGTGCATAT-----TTGTATGCTTCC 510
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 170 ValAsnPhe-----AspProAlaAlaPheThrGluAsnValPheHisSer 184

QY 511 AGAGTTATGCCAAGTCTCAATAGGTCAACAATCTTTTGTGGCACCACAAATGTGAAT 570
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 GlyArgSerThrGlyTyrGlySerPheGluSerTyrHisLeuGlyMetTyrCysProAsn 204

QY 571 GGTACACATCTGGT-----ACAATGGGTTCTCCAGTAGTAACGGTGACGTTGCT 621
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 GlyTyrPheLeuGlyGlyThrGluLysIleAspTyrAspSerSerAsnAsnValAsp 224

QY 622 ATTGATTGTCATAATATTCATATTTGGTATATACAAAAGGATTAAATGATTGGAATTC 691
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 LeuAspCysSerSerValGlnValTyrSerSerAsnAspPheAsnAspTrpTrpPhePro 244

QY 682 GTTTCATCTGAATCATTTAGTTACATAAATCTTGATCATCTAATCGAATTCAGATTAA 741
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 245 GlnSerTyrAsnAspThrAsnAlaAspValThrCysPheGlySerAsnLeuTrpIleThr 264

QY 742 TAT---CAAAATGTACCTGCTGTTATCGTCCATTTATTGATGCTTATATTTCT---GCT 795
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 LeuAspGluLysLeuTyrAspGlyGluMetLeuTrpValAsnAlaLeuGlnSerLeuPro 284

QY 796 ACAGATGTTAAACCAATATATCTTTAGCATATACCAATGATTATATCTTGT----- 843
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 AlaAsnValAsnThrIleAspHisAlaLeuGluPheGlnTyrThrCysLeuAspThrIle 304

QY 844 GCTGGCAGTCGCTGCAAAAGTAACCTTTCACATTTAAGA-----TGGACTGGA 891
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 305 AlaAsnThrThrTyrAlaThrGlnPheSerThrThrArgGluPheIleValTyrGlnGly 324

QY 892 TACAAGAAATAGTATCGCGGATCTAACGGTATTGTTCATTTGTCTACAACACTAGACAGTT 951
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 325 ArgAsnLeuGlyThrAlaSerAlaLysSerSerPheIleSerThrThrThrThrAspLeu 344

QY 952 ACAGAC-----AGTACCACCTGCTGTCACACTACTTTTACCAATTCATCAATCCA 993
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 ThrSerIleAsnThrSerAlaTyrSerThrGlySerIleSerThrVal----- 360

QY 994 AGTGTGATAAAACCAAAACAATCGAAATTTTCCAACTTATTCACACCACTACCATCACA 1053
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GluThrGlyAsnArgThrThrSerGluValIleSerHisValValThrThrSerThrLys 380

QY 1054 ACTTCATATGTTGGTGTGACTACTTCTATCTCACTAAAGACTGCACCAATTTGGTGAACA 1113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 381 LeuSerProThrAlaThrThrSerLeuThrIleAlaGlnThrSerIleTyrSerThrAsp 400

QY 1114 GCTACTGTTATTGTTGATGTGCCATATCATPACCAACA----- 1152
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 401 SerAsnIleThrValGlyThrAspIleHisThrThrSerGluValIleSerAspValGlu 420

QY 1153 ACTGTTACAGTGAATGACGAGCAACAACTACCACTACCACC---ACAACCTCGTACCAATCCA 1209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 ThrIleSerArgGluThrAlaSerThrValAlaAlaProThrSerThrThrGlyTrp 440

QY 1210 ACTGATTCAATTGCACAGTCAGTGGGTACAA 1239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 ThrGlyAlaMetAsnThrTyrIleSerGln 450
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RESULT 12

AB058564
ID AB058564 standard; protein; 800 AA.
XX AB058564;
XX 29-JUL-2004 (first entry)
XX Human genome derived single exon protein #4798.
XX Human; gene expression; single exon probe; microarray;


```
Db 298 SerPheThrSerSerThrValThrSerThrAlaSerThrHisThrThrAlaIleThrSer 317
      :::::|||||::: |||::: |||:::
Qy 865 AAACCTTTACATTTAAGATGACGTGGATACAAAGAAATAGTGGCGGATCTAACGGTATT 924
      ||| |||||
Db 318 ValProThrThrLeu-----GlyThr 324
      ||| |||||
Qy 925 GTCATTGTTGTACACTAGA----- 945
      :::::|||||:::
Db 325 MetValThrSerThrSerArgIleProSerThrValSerThrSerIleProThrSerGln 344
      ||| |||||
Qy 946 -----ACAGTTTACAGACAGTACCACTGCTGCTCACT---ACTTTACCAATTCACCAAGT 996
      ||| |||||
Db 345 ProIysThrValAsnSerSerSerGlyGlyIleThrGlySerLeuProMetMetThrAsp 364
      ||| |||||
Qy 997 GTTGATAAACCAAAACAAATCGAAATTTTGCACCTATTCACACCACTACCACTACCACT 1056
      ::: |||||:::
Db 365 LeuThrSerGlyTyrThrValSerSerMetSerAlaIleProThrThrValIleProThr 384
      ||| |||||
Qy 1057 TCA-----TATGTTGGTGTGACT----- 1074
      ||| |||||
Db 385 SerLeuThrValGlnAsnThrGluThrSerIlePheValSerMetThrSerAlaThrThr 404
      ||| |||||
Qy 1075 -----ACT 1077
      ||| |||||
Db 405 ProSerGlyArgProThrPheThrSerThrValAsnThrProThrArgSerLeuLeuThr 424
      ||| |||||
Qy 1078 TCCTATCTGACT-----AAGCTGCACCAATTTGGTGAACA 1113
      ||| |||||
Db 425 SerPheProThrThrHisLeuPheSerSerSerMetSerGluSerSerAlaGlyThrThr 444
      ||| |||||
Qy 1114 GCTACTGTTATTTGTTGATGTCATATCACTACTACCACTGTT-----ACCAGTCAA 1167
      ||| |||||
Db 445 HisThrGluSerIleSerSerProAlaThrThrSerThrLeuHisThrThrAlaGlu 464
      ||| |||||
Qy 1168 TGGACAGGACAACTACCTACCAACCACTCGTACCAATCCACT-----GATTCAATT 1221
      ||| |||||
Db 465 SerThrProSerCysThrThrThrThrSerPheIleThrSerThrMetGluProLeu 484
      ||| |||||
Qy 1222 GACACAGTGGTG 1233
      ||| |||||
Db 485 SerThrIleVal 488
      ||| |||||
RESULT 14
ABG66702
ID ABG66702 standard; protein; 1296 AA.
XX AC ABG66702;
XX XX
XX 30-AUG-2002 (first entry)
XX DE Human novel polypeptide #37.
XX KW Human; inflammatory condition; shock; sepsis; immune response; cancer;
XX KW wound healing; central nervous system disease; haematopoiesis;
XX KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
XX KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
XX KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
XX KW bone degenerative disorder; periodontal disease; reperfusion injury;
XX KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
XX KW allergic condition; thrombolysis; thrombosis; coagulation disorder;
XX OS Homo sapiens.
XX XX
XX PN WO200244340-A2.
XX PD 06-JUN-2002.
XX XX
XX PF 30-NOV-2001; 2001WO-US047004.
XX XX
XX PR 30-NOV-2000; 2000US-00728952.
XX XX
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PA (HYSB-) HYSEQ INC.
XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
PI Yamazaki V, Ujwal ML, Drmanac RT;
XX WPI; 2002-508509/54.
DR N-PSDB; ABK94926.
XX Novel nucleic acids and polypeptides for diagnosis, treatment of
PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
PT disorders, cancer and promoting wound healing.
XX Claim 10; Page 604-607; 672pp; English.
XX The invention relates to human novel polynucleotides and associated
CC polypeptides. The polynucleotides and polypeptides are useful for
CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
CC and cancer and for promoting wound healing. The sequences are used to
CC induce the proliferation of neural cells and regeneration of nerve and
CC brain tissue, and are useful for the treatment of central and peripheral
CC nervous system diseases and neuropathies, such as Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and amyotrophic lateral
CC sclerosis. The sequences are involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
CC cell disorders and platelet disorders such as thrombocytopenia,
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC disease. The sequences of the invention are also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
CC gravis, allergic conditions such as asthma, thrombolysis or thrombosis
CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human
CC novel polypeptides of the invention
XX SQ Sequence 1296 AA;
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Alignment Scores:
Pred. No.: 1.25e-07 Length: 1296
Score: 179.00 Matches: 116
Percent Similarity: 35.11% Conservative: 68
Best Local Similarity: 22.14% Mismatches: 164
Query Match: 7.73% Indels: 176
DB: 5 Gaps: 24
US-09-715-876-7_COPY_52_1296 (1-1245) x ABG66702 (1-1296)
Qy 4 ACAATCACTGGTGGTTTTGTAGATGTTT-----AATTCATTAACTGGTCCAAT 51
      ||| |||||
Db 27 ThrIleProSerValArgProThrPheThrSerThrHisAsnThrLeuThrSerSerLeu 46
      ||| |||||
Qy 52 GCTGCTAATATGCTTTCAAAGGCCAGGATACCAACTTGGAAATGCTGTTTGGTTGG 111
      ||| |||||
Db 47 LeuThrThrPhe-----ProGlyThrTyrSerPheSerSerMetSerAla 62
      ||| |||||
Qy 112 TCCTTAGATGGTACC-----AGTGCCAATCCAGGGGATACATTCACA 153
      ||| |||||
Db 63 SerSerAspGlyThrThrHisThrGluThrIleThrSerLeuProAlaSerThrSerThr 82
      ||| |||||
Qy 154 TTGAATATGCCATGT-----GTGTTTAATATATACTACTTCA 189
      ||| |||||
Db 83 LeuHisThrThrAlaGluSerThrThrAlaHisThrThrThrSerPheThrThrSer 102
      ||| |||||
Qy 190 CAACACA-----TCTGTTGATTTAAGTCCGATGGTGTAAATATGCT 231
      ||| |||||
Db 103 ThrThrMetGluSerProSerSerSerValAlaThrThrSerThrGly-----Gln 119
      ||| |||||
Qy 232 ACTTGTCAATTTTATTTCTGGTGAAGAATTCACAACTTTTCTACATTAACATGTAATGCTG 291
      ||| |||||
Db 120 ThrThrPheSerSerSerThrAlaThrPheThrGluThrThrLeuThrThrProThr--- 138
```


CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1322 AA;

Alignment Scores:
 Pred. No.: 1.96e-07 Length: 1322
 Score: 177.00 Matches: 112
 Percent Similarity: 34.38% Conservative: 53
 Best Local Similarity: 23.33% Mismatches: 181
 Query Match: 7.71% Indels: 134
 DB: 8 Gaps: 26

US-09-715-876-7_COPY_52_1296 (1-1245) x ADN18700 (1-1322)

Qy 58 AATTATGCTTTCAAGGCCAGGATACCACTTGGATGCTGTTTGGGT---TGGTCC 114
 Db 104 AsnTrpGlyCysIleGlyAlaCysSerAsnAsnProIleIleAlaTyTrpSer 123
 Qy 115 TTAGAT-----GGTACCAGTCCCAATCCAGGGATACATTACATGAATATG----- 162
 Db 124 ThrAspLeuPheGlyPheTyThrThrProThrAsnVal---ThrLeuGluMetThrGly 142
 Qy 163 -----CCATGTGTGTTTAAATACTACTTCTCAACCAATCT 198
 Db 143 TyrPheLeuProGlnThrGlySerTyThrPheLysPheAlaThrValAspAspSer 162
 Qy 199 GTTGATTTAACTGCGGATGTT---GTTAAATATGCTACTTGTCTCAATTTATCTGGTCAA 255
 Db 163 AlaIleLeuSerValGlyGlySerIleAlaPheGluCysCys-----AlaGln 178
 Qy 256 GAATTCACAACTTTTTCACATTAAACATGCTACTGTGAACGACGCTTTGAAATCATCCATT 315
 Db 179 GluGlnProIleThrSerThrAsnPheThrIleAsn-----GlyIle 193
 Qy 316 AAGGCATT-----GGTACAGTT----- 333
 Db 194 LysProTrpAsnGlySerProProAspAsnIleThrGlyThrValTyMetTyrAlaGly 213
 Qy 334 -----AspAsnLeuSer-----ACTTTACCAATT 345
 Db 214 PheTyTrpProMetLysIleValTySerAsnAlaValAlaTrpGlyThrLeuProIle 233
 Qy 346 GCATTCATATGTT---GGTGGAAACAGTTTCATCACTGATTTGGAGATTTCTAAATGTTT 402
 Db 234 SerValThrLeuProAspGlyThrThrValSerAspAspPheGluGly----- 249
 Qy 403 ACTGCTGTACCAATACAGTCACATTAAATGATGGTGATGAAGATATCTCAATTGATGTT 462
 Db 250 -----TyValTyThrPhe-----AspAsnLeuSer----- 259
 Qy 463 GAGTTTGAAGAGTCAACCGTTGATCCAAAGTCGATTTGTTGATGCTTCCAGATGATGCCA 522
 Db 260 GlnProAsnCysThrIleProAspProSerAsnTyThr---ValSerThrThrIleThr 278
 Qy 523 AGTCTCAATAGGTCCACAACTCTTTTGTGGCACCACCAATGTGAAAATGGTTACACATCT 582
 Db 279 ThrThrGluProTrpThrGlyThrPheThrSerThrSerThrGluMetThrThrValThr 298
 Qy 583 GGTACAAATGGGGTCTTCCAGTAGTAACGGTGAAGTGTGCTATTGATTTGCTCAAAATATCAT 642
 Db 299 GlyThrAsnGlyValProThrAspGluThrValIleValIleArgThrProThrThrAla 318
 Qy 643 ATTGGTATCAGAAAAGGATTAATGATTTGGAATATTCGGTTTCACTGAATCATTTAGT 702
 Db 319 SerThrIleIleThrThrThrGluProTrpAsnSerThrPheThrSerThrSerThrGlu 338
 Qy 703 TACACTAAACTTGTACATCTTAATGGAATTCAGATTAAATATCAAAATGTACCTGCTGCT 762

Db 339 LeuThrThrValThrGlyThrAsnGlyValArgThrAspGluThrIleIle--- 355
 Qy 763 TATCGTCCATTTATTCATGCTTATATTTCTGTACAGATGTTAAACCAATATATCTTTAGCA 822
 Db 356 -----ValIleArgThrProThrThrAlaThrThrAlaIleThrThrGluPro 372
 Qy 823 TATACCAATGATTTATCTGTGCTGGCAGTCGCTGCAAAAGTAAACCTTTTCACCTTTAAGA 882
 Db 373 TrpAsnSerThrPheThrSerThrSerThrGluLeu----- 384
 Qy 883 TGGACTGGATACAGAATAGTATGTCGGATCTAAACGGTATT-----GTCATTGTT 933
 Db 385 -----ThrThrValThrGlyThrAsnGlyLeuProThrAspGluThrIle 399
 Qy 934 GCTACAACTAGAACAGTACAGACAGTACCACCTGTCTCTACTACTTTA---CCATTCAT 990
 Db 400 IleValIleArgThrProThrThrAlaThrThrAlaMetThrThrThrGlnProTrpAsn 419
 Qy 991 CCAAGTGTTCATAAAACCAAAACA----- 1014
 Db 420 AspThrPheThrSerThrSerThrGluLeuThrThrValThrGlyThrAsnGlyLeuPro 439
 Qy 1015 -----ATCGAAATTTTGCACCTTATCCAAACCACTACATCACAACCT--- 1056
 Db 440 ThrAspGluThrIleValIleArgThrProThrThrAlaThrThrAlaMetThrThr 459
 Qy 1057 -----TCATATGTTGGTGTGACTACTTCTATCTGACTTAACACTGCA 1098
 Db 460 ThrGlnProTrpAsnAspThrPheThrSerThrSerThrGluLeuThrThrValThrGly 479
 Qy 1099 -----CCAATTGGTGAACACAGTACTGTTTATTTGTTGATGTCCTATATCATACT 1146
 Db 480 ThrAsnGlyLeuProThrAspGluThr---IleIleValIleArgThrProThrThrAla 498
 Qy 1147 ACCACA-----ACTGTTACAGTGAATGGACAGGAACAATCACT----- 1185
 Db 499 ThrThrAlaMetThrThrThrGlnProTrpAsnAspThrPheThrSerThrSerThrGlu 518
 Qy 1186 ---ACCACCACTCGTACCCT---CCAACTGATTCAATTCACACAGTGGTGGTA 1236
 Db 519 IleThrThrValThrGlyThrAsnGlyLeuProThrAsp-----GluThrIleIleVal 536

Search completed: September 8, 2005, 17:41:09
 Job time : 227 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:52:54 ; Search time 3078 Seconds
(without alignments)

15396.366 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296

Perfect score: 1245

Sequence: 1 aagacaatcactggtgtttt.....cagtggtggtacaagtcca 1245

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hnc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_g881.*

9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	155	12.4	1047	9	CNS07D6L
2	152.8	12.3	560	6	CD085816
3	139.4	11.2	1011	9	CNS07DAY
C 4	121.2	9.7	1050	9	CNS07CMQ
5	82.6	6.6	525	8	BZ351620
C 6	80.4	6.5	735	9	CNS04NSM
7	80.2	6.4	843	8	BZ643413
8	78.4	6.3	501	9	FR0048173
9	77.8	6.2	619	9	CG372306
10	77.6	6.2	513	8	BZ423698
11	76.6	6.2	773	9	CNS01VTG
12	75.8	6.1	480	8	BZ643398
13	75.2	6.0	694	8	BH355163
14	71.8	5.8	494	9	FR0048073
C 15	69.8	5.6	427	8	BZ423231
16	69.6	5.6	350	8	BH879665
17	69.6	5.6	989	9	CNS02HA4
18	68.6	5.5	334	8	BZ614791
19	68.4	5.5	395	8	BZ316940
20	67.8	5.4	989	8	CC149236
21	67.6	5.4	356	8	CC171914
22	66.8	5.4	699	5	BK729701
23	66.6	5.3	423	8	BZ309688
24	66.6	5.3	933	8	AZ204694

C 25	65.8	5.3	530	8	AZ166409	AZ166409 SP_0088_A
26	65.4	5.3	306	8	BZ375744	BZ375744 ie61b04.g
C 27	65	5.2	528	6	CD336470	CD336470 StrPu537.
28	64.8	5.2	311	8	BZ638753	BZ638753 OGCAx82TM
29	64.6	5.2	320	8	BZ314341	BZ314341 h216b12.b
30	64	5.1	305	8	BZ333772	BZ333772 h27h02.g
31	63.6	5.1	428	5	BQ036742	BQ036742 SS2-0450
32	63.4	5.1	621	8	AZ164800	AZ164800 SP_0076_B
33	62.6	5.0	914	8	AZ205202	AZ205202 SP_0100_A
C 34	62.4	5.0	810	8	AZ199472	AZ199472 SP_1039_B
35	62.2	5.0	788	8	AZ183942	AZ183942 SP_1002_B
36	62	5.0	280	9	CG218306	CG218306 OGTX57TH
37	61.8	5.0	266	8	BZ313584	BZ313584 h209b05.b
38	61.6	4.9	287	8	BZ644508	BZ644508 OGCBP93TM
39	61.2	4.9	619	9	FR0047601	AL444386 Fugu rubr
40	60.8	4.9	550	9	FR0043207	AL130699 Fugu rubr
41	60.4	4.9	450	9	FR0025683	AL018519 F. rubripe
42	59.8	4.8	922	7	CK411084	CK411084 AUF_1phdk
43	59.6	4.8	320	8	CC167070	CC167070 i158a04.g
C 44	59.4	4.8	469	9	CL569187	CL569187 4-12-4 Ma
45	59.4	4.8	798	2	BF936821	BF936821 EST459876

ALIGNMENTS

RESULT 1
CNS07D6L/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS07D6L 1047 bp DNA linear GSS 08-JUL-2001
T7 end of clone BD0AA009H06 of library BD0AA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.

AL440083 1 GI:12223494

GSS

Candida tropicalis

Candida tropicalis

Rukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; mitosporic Saccharomycetales; Candida.

1 (bases 1 to 1047)

Souciat,J.L., Aigle,M., Artiguenave,P., Blandin,G.,

Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,

Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,

Saurin,W., Tekaiia,P., Toffano-Nioche,C., Wesolowski-Louvel,M.,

Wincker,P. and Weissbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

FEBS Lett. 487 (1), 3-12 (2000)

20584711

11152876

2 (bases 1 to 1047)

Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,P. and

Dujon,B.

Genomic exploration of the hemiascomycetous yeasts: 16. Candida

tropicalis

FEBS Lett. 487 (1), 91-94 (2000)

20584726

11152891

3 (bases 1 to 1047)

Genoscope.

Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY Cedex, FRANCE. [E-mail :

seqref@genoscope.cns.fr Web :

This GSS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to

5 kb were prepared and both extremities were sequenced. See

keywords for description of this sequence and for the sequence of

the other extremity of this insert.

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FEATURES             Location/Qualifiers
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                        /organism="Candida tropicalis"
                        /mol_type="genomic DNA"
                        /strain="CBS 94"
                        /db_xref="taxon:5482"
                        /clone="BD0AA009H06"
                        /clone_lib="BD0AA"
                        /note="end : T7"
     misc_feature      complement(<2..>484)
                        /note="similar to O74660 [ Agglutinin-like protein 4
                        precursor, ALS4 ] [ Candida albicans] "
                        /evidence="not experimental"

```

ORIGIN

Query Match	12.4%	Score 155;	DB 9;	Length 1047;
Best Local Similarity	62.1%;	Pred. No. le-27;		
Matches 264;	Conservative	0;	Mismatches 155;	Indels 6;
Gaps 1;				

Qy	7	ATCACTCGTGT	TTTTGATAGT	TTTAATTCATTA	CTTGGTCCA	ATGCTGCTAA	TT-----	61		
Db	427	ATACTCGGGAT	TTTTTATT	TGGTTCCGAT	TCATTAACAT	GGAATGCTG	CTCGGNTT	ACCC 368		
Qy	62	-ATGCTTTCAA	AGGGCCAGAG	TACCCAACT	TGGAACTG	CTGTTTGGG	TGTGCTCT	TAGAT 120		
Db	367	AGTGCA	TACCAAGT	CCACAAT	TCCTAC	CTGGACT	CGAGAA	CTAA	CAATGGT	TTTTTGAAT 308
Qy	121	GGTACCA	GTGCCAAT	CCAGGGGAT	ACATTC	ACATGAA	TATGCC	ATGTGTG	TTTAAATAT 180	
Db	307	GGAGA	CTCTG	TGAACCA	AGGTGAT	ACATTC	CAATTAAT	ATG	CCATGTGTAT	TTCAAAGTTC 248
Qy	181	ACTACT	TTCAAAA	CATCTG	TTGATTTAA	CTCCGAT	GTGTAA	ATAATG	CTACTT	GTGTGTCAA 240
Db	247	ATTA	CAAAATCA	AAACACTG	TTGATTTG	ATCTG	CTGATG	CACTCT	TATGCA	CTGTATAT 188
Qy	241	TTTTTAT	CTCGTGA	GAAGAA	TTCA	CAACTTTTT	CTCATTTAA	CAATG	CTACTGTG	GAACGACGCT 300
Db	187	CTCA	ATTTCTG	GAGAAGA	AAATTTACT	ACTTTTCT	CAAGTTTAA	AGCTGT	ACTGTG	TTTCATCTACC 128
Qy	301	TTGAAAT	CATCCAT	TAAAGCA	TTTGGT	ACAGT	TACTTTAC	CAAT	TGCATTC	CAAGTTGGT 360
Db	127	TTG	CAACATAT	ATCCCA	AGCTCG	TGGTACT	TTACATG	TTCTCT	TTGACAT	TTAATGTGGGT 68
Qy	361	GGAA	CAGGTT	CATCAA	CTGATTT	CGGAAGAT	TTCTAA	ATGTTTTT	ACTGCTG	TGTAACCAATACA 420
Db	67	AGTT	CGGAACT	CTCTG	TTTCTG	TGACTG	ATTCTACT	TTGCTT	CAGAC	CAAGGTGTAACACA 8
Qy	421	GTCA	C 425							
Db	7	GTA	C 3							

RESULT 2	CD085816	560 bp	linear	EST 14-SEP-2003
LOCUS	MC1-0021P-A069-G05-U.B	MC1-0021	Schistosoma mansoni	CDNA clone
DEFINITION	MC1-0021P-A069-G05.B.	MC1-0021P-A069-G05.B.	MC1-0021P-A069-G05.B.	MC1-0021P-A069-G05.B. mRNA sequence.

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
CD085816.1	GI:14636773	EST.	<i>Schistosoma mansoni</i>	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.	1 (bases 1 to 560)
			<i>Schistosoma mansoni</i>		Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Otjof, E.P.B., Paquela, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweiler, P.P., Reis, E.M., Ribeiro, M.A., Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,

TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E. Transcriptome analysis of the acelomate human parasite <i>Schistosoma mansoni</i>	Nat. Genet. 35 (2), 148-157 (2003)	22879926	12973350	Contact: Dr. Sergio Vertovski-Almeida Departamento de Bioquímica Instituto de Química - Universidade de São Paulo Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP, Brasil Tel: +55-11-3091-2173 Fax: +55-11-3091-2186 Email: verto@ic.usp.br

This sequence was derived from the FAFESP Schistosoma mansoni EST
 Email: verjow@iq.usp.br
 Genome Project. All sequences in the project were assembled and
 annotated. This entry and all the assembled sequences can be seen
 in the following URL <http://bioinfo.iq.usp.br/schisto/>
 Plate: MC1-0021P-A069 row: 5 column: G.

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FEATURES
source
Location/Qualifiers
1..560
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MC1-0021P-A069-G05.B"
/sex="mixed pool"
/dev_stage="Cercaria"
/lab_host="Biomphalaria glabrata"
/clone_lib="MC1-0021"
/note="Vector: pGEM T-easy"

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ORIGIN

Query Match 12.3%; Score 152.8; DB 6; Length 560;
Best Local Similarity 61.6%; Pred. NO. 3.1e-27;
Matches 244: Conservative 0; Mismatches 152; Indels 0;
Gaps 0;

Qy	76	CAAGGATACCCAACTTGGGAATGCTGTTTTGGGTTGGTCTTAGATCGTACCGATGCCAAT	135
Db	9	CTGCGACGCCCAAGTTGGATTTGCAACTTATCTCTGGAAGATTTTGGGCTCAAAACGTGCAT	68
Qy	136	CAAGGGGATACATTTCACTATTGAATATGCCATGTGTTTTAAATATATCTCTCACAAACA	195
Db	69	CTGGTGATACCTTTTACTTTTAAATATAGCCCTGTGTGTTTTCAAGTTTACCACCTCAAGAC	128
Qy	196	TCCTGTTGATTTAACTCCCGATGGTGTTTAAATATGCTACTTGTGCAATTTTATTCTGGTGAA	255
Db	129	AGCGTCGACTTAACGGTTGCGGATACTGTTTATGCTACTTGTCAAATTTGCTCTCGGTGAT	188
Qy	256	GAAATTACAACTTTTTTCTACATTTAACTATGACTGTGTGAAACGACGCTTTTGAATCATCCATT	315
Db	189	TTAGTTGTGTTGCTTACTCCCAATTTAAAGTGTACTGCTAGTTAAACAAATGTTAAAGCAAGACA	248
Qy	316	AGGCGATTTGGTACAGTTACTTTTACCAAATTTGCATTCAAATGTTGGTGGGAAACAGGTTTCATCA	375
Db	249	AATGCTGCTGGTTCTGTTCAATTTTCTATTGCTTTTCAACGTTGGGGGATCAGCAAAATTCCT	308
Qy	376	ACTGATTTGGGAAGATCTTAAATGTTTTTACTGCTGGTACCAATACAGTTCACATTTAATGAT	435
Db	309	GTGCAATTCAAAAATTTCCCAATGTTTTACCGCTGGTTCCAAACCAAGTTACATTCACCTGAC	368
Qy	436	GGTGATAAAGATATCTCAATTTGATGTGATTTGAA	471
Db	369	GGTGACAAGAGTTGACTACCAAGCAAACTTTCAA	404

RESULT 3	CNS07DAY	1011 bp	DNA	linear	GSS 08-JUL-2001
CNS07DAY					
LOCUS					
DEFINITION	T7 end of clone BD0AA010H12 of library BD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence.				
ACCESSION	AL440240				
VERSION	AL440240.1	GI:12223651			


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KEYWORDS      GSS.
SOURCE         Candida tropicalis
ORGANISM       Candida tropicalis
REFERENCE      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
AUTHORS        Saccharomycetales; mitosporic Saccharomycetales; Candida.
               1 (bases 1 to 1011)
               Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
               Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
               de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
               Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
               Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
               Wincker,P. and Weissenbach,J.
               Genomic exploration of the hemiascomycetous yeasts: 1. A set of
               yeast species for molecular evolution studies
               FEBS Lett. 487 (1), 3-12 (2000)

TITLE          Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL        yeast species for molecular evolution studies
MEDLINE        20584711
PUBMED         11152876
REFERENCE      2 (bases 1 to 1011)
AUTHORS        Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
               Dujon,B.
               Genomic exploration of the hemiascomycetous yeasts: 16. Candida
               tropicalis
               FEBS Lett. 487 (1), 91-94 (2000)
               11152891
               3 (bases 1 to 1011)
               Genoscope.
               Direct Submission
               Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
               2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
               seqref@genoscope.cns.fr - Web :
               This GSS is part of a random genomic sequencing program of thirteen
               yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
               exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
               Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
               lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
               angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
               Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
               5 kb were prepared and both extremities were sequenced. See
               keywords for description of this sequence and for the sequence of
               the other extremity of this insert.
               Location/Qualifiers
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               /organism="Candida tropicalis"
               /mol_type="genomic DNA"
               /strain="CBS 94"
               /db_xref="taxon:5482"
               /clone="BD0AA010H12"
               /clone_lib="BD0AA"
               /note="end : 77"
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               /note="similar to P46590 [ Agglutinin-like protein 1
               precursor, AL51 ] [ Candida albicans]
               1 putative frameshift(s)"
               /evidence=not_experimental

misc_feature

ORIGIN
Query Match      11.2%; Score 139.4; DB 9; Length 1011;
Best Local Similarity 65.0%; Pred. No. 7.9e-24;
Matches 214; Conservative 4; Mismatches 110; Indels 1; Gaps 1;

QY 1 AAGACAATCACTGGTGTGTTTGGATGATGTTTAACTTAATCTGTGTCCTCAATGCTGCTAAT 60
DB 670 AAAGAAATTCGCGGTGTGTTTCATAGGATTTGAATCTTAACTTGGGATAAAGCTGGTGAAT 729
QY 61 TATGCTTTCAAGAGCCAGGATACCACACTTGGATGCTGTTTGGGTGGTCTCTTAGAT 120
DB 730 TATGATATCAAGGTCCTCAATATCCATCATGGAATGCGGTGTTGATGTTGCTGTAGAT 789
QY 121 GGTACCAGTGCCAAATCCAGGGGATACATTCACATTTGAATATGCCAATGTTGTTTAAATAT 180
DB 790 GGCACAACACATCCCCAGGTGATAGGTTCACTTTTGATCATGCCCTGCTCTTCAAGTTC 849

```

```

QY 181 ACTACTTCACAAACATCTGTGTGATTTAACTGCGATGGTGTAAATATGCTACTTGTCAA 240
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
850 ACTAGGTYTGCAVTTCTGTGTGGATCTGACTGCGAATGGKATGACATATGCCACATGTGAT 909
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
241 TTTTAT-TCGGTGAAGAATTCAACACTTTTCTACATTAACATGTAATGCTGTAACGACGC 299
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
910 CTTTCATGCKKGGTGAAGAGTTTACTACTTACTCTAGTTTACGCTGTAATGCTCTAYAGATTC 969
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
300 TTGAAATCATCCATTAAAGGCAATTGGTA 328
870 GTTAAGTCTGTTTCATGAGCTATGGGATA 998

RESULT 4
CNS07CMQ/c      1050 bp      DNA      linear      GSS 08-JUL-2001
LOCUS           T7 end of clone BD0AA004B02 of library BD0AA from strain CBS 94 of
DEFINITION      Candida tropicalis, genomic survey sequence.
ACCESSION       AL439368
VERSION         AL439368.1 GI:12222781
KEYWORDS        GSS.
SOURCE          Candida tropicalis
ORGANISM        Candida tropicalis
REFERENCE       Rukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
AUTHORS         Saccharomycetales; mitosporic Saccharomycetales; Candida.
               1 (bases 1 to 1050)
               Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
               Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
               de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
               Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
               Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
               Wincker,P. and Weissenbach,J.
               Genomic exploration of the hemiascomycetous yeasts: 1. A set of
               yeast species for molecular evolution studies
               FEBS Lett. 487 (1), 3-12 (2000)
               20584711
               11152876
               2 (bases 1 to 1050)
               Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
               Dujon,B.
               Genomic exploration of the hemiascomycetous yeasts: 16. Candida
               tropicalis
               FEBS Lett. 487 (1), 91-94 (2000)
               11152891
               3 (bases 1 to 1050)
               Genoscope.
               Direct Submission
               Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
               2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
               seqref@genoscope.cns.fr - Web :
               This GSS is part of a random genomic sequencing program of thirteen
               yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
               exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
               Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
               lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
               angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
               Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
               5 kb were prepared and both extremities were sequenced. See
               keywords for description of this sequence and for the sequence of
               the other extremity of this insert.
               Location/Qualifiers
               1..1050
               /organism="Candida tropicalis"
               /mol_type="genomic DNA"
               /strain="CBS 94"
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               /clone_lib="BD0AA"
               /note="end : 77"
               complement(<7..>921)
               /note="similar to O13368 [ Agglutinin-like protein ALA1
               precursor ] [ Candida albicans]"

misc_feature

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AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 735)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES Location/Qualifiers
source
1..735
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="123M05"
/clone_lib="G"
/note="Genoscope sequence ID : COBG123AG03LP1-end : T7"

ORIGIN
Query Match 6.5%; Score 80.4; DB 9; Length 735;
Best Local Similarity 47.4%; Pred. No. 4.4e-09;
Matches 251; Conservative 6; Mismatches 272; Indels 1; Gaps 1;
Qy 699 TAGTTACACTAAACTGTGATCATCTATGGAATTCAGATTAATCAAAATGTACCTGC 758
Db 530 TACTGCTAAACTACTGCTACTACTGCGACTCTACTACTGCTACWATTKCWC 471
Qy 759 TGGTTATGCTCCATTTATTTGATGCTTATATTTCTGCTACAGATGTTAAACCAATATACTTT 818
Db 470 TGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 411
Qy 819 AGCATATACCAATGATTATATCTTGCTGGCAGTCTGCTGCAAGTAAACCTTTTACCTTT 878
Db 410 TGCTACTACTACTGCTGCTACTACTGCTGCTGCTACTACKGCKTGTCTACTACTACTAC 351
Qy 879 AAGATGGAGTGGATACAGAATAGTATGATGCGGATCTAACGGTATTTGTCATTTGTCTAC 938
Db 350 TACTACTACTTTTCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 291
Qy 939 AACTAGACACTTACAGACACTACACCTGCTGCTGCTACTTTTACCATTCAATCCAAGTGT 998
Db 290 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTGCT 231
Qy 999 TGATAAAACCAAAACAAATTCGAAATTTTCCAACTTATTCACACCTACTACCACTTC 1058
Db 230 TACTGCTGCTACTACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTGCT 171
Qy 1059 ATATGTTGGTGTGACTTCTCTATCTGACTAAGAGTGCACCAATTTGGTGAACAGCTAC 1118
Db 170 TACTGCTGCTACTACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 111
Qy 1119 TGTATTTGTTGATGTCATATCA-TACTACCACAACTGTTACCAGTGAATGGACAGAA 1177
Db 110 TACTACTGCTGCTACTACTACTACTACTACTACTGCTGCTACTACTGCTACTACTACTGCTA 51
Qy 1178 CAATCACTACCACCACTCGTACCAATCCAACTGATTCATTAATTGACACA 1227
Db 50 CTA 1

RESULT 7
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DEFINITION OGAOW57M ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma011J17,

ACCESSION B2643413
VERSION B2643413.1
KEYWORDS GI:28104915
SOURCE Zea mays
ORGANISM Zea mays

genomic survey sequence.
B2643413
B2643413.1 GI:28104915
GSS.
Zea mays

Zeakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 843)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGAOW57TC
Contact: Cathy Whitelaw
TIGR

7912 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..843
/organism="Zea mays"
/mol_type="genomic DNA"
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/note="Vector: pBCSk-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Other_GSSs: OGAOW57TC
Contact: Cathy Whitelaw
TIGR

7912 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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/note="Vector: pBCSk-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES Location/Qualifiers
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methylation filtered genomic DNA library"

ORIGIN

Query Match 6.4%; Score 80.2; DB 8; Length 843;
Best Local Similarity 45.7%; Pred. No. 5e-09;
Matches 280; Conservative 0; Mismatches 333; Indels 0; Gaps 0;
Qy 616 GTTGCTATTGATGCTCAAAATATTCATATTTGGTATCACAAAGATTTAAATGATGGAT 675
Db 792 GCTACTACTGCTACTACTGCTGCTGATGCTGCTACTGCTACTGCTACTGCTACTGCTACT 733
Qy 676 TATCCGGTTTCATCTGATCATTTAGTTACATAAACTTTGTACATCTTAATGGAATTCAG 735
Db 732 ACTGCTACTGCTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACT 673
Qy 736 ATTAATATCAAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
Db 672 ACTACTGCTACTGCTGCTACTACTACTACTACTACTACTGCTACTGCTGCTACTGCTGCT 613
Qy 796 ACAGATTTAACCAATATACCTTTAGCATATACCAATGATTATATCTTGTGCGCAGTCGT 855
Db 612 ACTGCTGCTATTGCTGCTACTCCAGCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTACT 553
Qy 856 CTGCAAGTAAACCTTTTACCTTTAAGATGAGTGGATACAGATAGTATGATCGCGATCT 915
Db 552 GCTACTGCTGCTACTGCTGCTGCTACTACTGCTGCTACTGCTGCTACTGCTACTACTACT 493
Qy 916 AACGGTATTCATTTGTTGCTACAACTAGAACAGTTACAGACAGTACACACTGCTGCTACT 975
Db 492 GCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACTACTACT 433
Qy 976 ACTTTTACATTCATCCAGTGTGTGATTAACCAAAACAATCGAAATTTTGCACCTATT 1035
Db 432 GCTGCTGCTACTACTACTGCTGCTGCTACTACTACTACTACTGCTGCTACTACTACTACT 373
Qy 1036 CCACACCTACCATCACAACTTCATATGTTGGTGTGACTACTTCTTATCTGACTAAGACT 1095
Db 372 GCTCCTACTACTGCTACTACTGCTACTGCTGCTTCTACTACTACTGCTACTGCTACTGCT 313
Qy 1096 GCACCAATTGGTGAACAGCTACTGTTATTGTTGATGCGCATATCATACTACCACAACT 1155

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Db      312 ACTGCTACTGCTACAGCTACTACAGCTACTACTGCTACTCTGCTACTACTGCTACT 253
QY      1156 GTTACCGTGAATGGACGAGCAATACACTACACCACTGTTGTTACCAATCAACTGAT 1215
Db      252 ACTACTACTGCTACTACTGCTACTACTACTGCTACTACTGCTACTACTGCTACTGCT 193
QY      1216 TCAATTGACACAG 1228
Db      192 ACTGCTGCTACTG 180

RESULT 8
PRO048173
LOCUS      501 bp      DNA      linear      GSS 05-JAN-2001
DEFINITION Fugu rubripes GSS sequence, clone 264E22ca9, genomic survey
sequence.
ACCESSION  AL444958
VERSION     1 GI:12053458
KEYWORDS    GSS; genome survey sequence.
SOURCE      Takifugu rubripes (Fugu rubripes)
ORGANISM    Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodontidae; Takifugu.
REFERENCE   1 (bases 1 to 501)
AUTHORS     Clark,M.S.
TITLE       Direct Submission
JOURNAL     Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. UK Email:
            biohelp@hmp.mrc.ac.uk
COMMENT     Vector: pBluescript II KS
            V-type: phagemid
            PRIMER: KS
            DESC: One pass dye-terminator sequencing of BAC (pBelobACII) cloned
            genomic sequence
            The BACs can be obtained from http://www.incyte.com.

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Best Local Similarity 47.9%; Pred. No. 1.3e-08;
Matches 226; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

QY      755 CTGCTGTTATCGTCCTATTTATGATGCTTATATTTCTGCTACAGATGTTAACCAATATA 814
Db      19 CTGCTGCTTCTACTACTGCTACTACTACTACTACTGCTACTACTGCTGCTTCTACTA 78
QY      815 CTTTAGCATATACCAATGATATATCTTGTGCTGCAGTCGCTCGCAAGTAAACCTTTCA 874
Db      79 CTACTACTACTACTGCTACTACTACTACTGCTACTACTACTACTACTACTACTGCTG 138
QY      875 CTTTAAAGATGACTGGATACAGAATAGTATGTCGGGATCTAACGGTATTGTTCATTGTTG 934
Db      139 CTGCTTCTACTACTGCTACTACTACTACTACTGCTACTACTGCTGCTTCTACTACTA 198
QY      935 CTACAACTAGAACAGTTACAGACAGTACCCTACTGCTGTCACTACTTTACCATTCATCAAA 994
Db      199 CTACTACTACTACTACTACTACTACTACTACTGCTGCTACTACTACTACTACTACTACTA 258
QY      995 GTGTTGATAAAACCAAAACCAATCGAAATTTTGCAACCTATTTCCAACCACTACCATCAAA 1054
Db      259 CTACTACTACTACTACTGCTGCTACTACTACTACTGCTACTACTACTACTACTACTG 318
QY      1055 CTTTCATATGTTGGTGTGACTACTTCTCTATCTGACTAAGCTACGCCAAATGGTGAAACAG 1114

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Db      319 CTTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTGCTGCTTCTACTGCTA 378
QY      1115 CTACTGTTATTTGATGTCATATCATATACCACTACCACTGTTTACCACTGAATGGACAG 1174
Db      379 CTACTACTACTACTACTACTACTACTGCTACTACTACTACTACTACTACTGCTACTACTG 438
QY      1175 GAACATCATCTACCACCACTCGTACCAATCCAACTCAATCAATGTGACAC 1226
Db      439 CTGCTACTACTACTACTACTGCTAGTAGTACTACTACTACTACTACTACTACTACTAC 490

RESULT 9
CG372306      619 bp      DNA      linear      GSS 26-AUG-2003
LOCUS      OG4BI087C ZM_0.7_1.5_KB Zea mays genomic clone ZMBMa0811B15,
DEFINITION genomic survey sequence.
ACCESSION  CG372306
VERSION     1 GI:34289573
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 619)
AUTHORS     Whitelaw,C.A.; Quackenbush,J.; Van Aken,S.; Utterback,T.;
            Resnick,A.; Fraser,C.M.; Budiman,M.A.; Bedell,J.A.; Rohlfing,T.;
            Citek,R.W.; Nunberg,A.; Robbins,D. and Lakey,N.
            Consortium for Maize Genomics
            Unpublished (2002)
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.

FEATURES             Location/Qualifiers
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                /clone_lib="ZM_0.7_1.5_KB"
                /note="Vector: pBC5K; Site 1: HincII; 0.7-1.5 kb
                methylation filtered genomic DNA library"

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Query Match      6.2%; Score 77.8; DB 9; Length 619;
Best Local Similarity 47.8%; Pred. No. 1.9e-08;
Matches 226; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

QY      750 TGTACCTGCTGTTATCGTCCATTATTATGATGCTTATATTTCTGCTACAGATGTTAACCA 809
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QY      810 ATATATTTAGCATATACCAATGATATATCTTGTGTCGCGAGTCGTCGAAAGTAAACC 869
Db      113 TGCTACTACTACTACTACTACTACTCTCTACTACTACTACTACTACTACTACTACTACTAC 172
QY      870 TTTTCACTTTAAGATGACTGGATACAGATAGTATGTCGGGATCTAACGGTATTGTTCAT 929
Db      173 TACTACTACTACTACTACTACTACTACTACTGCTGCTGCTGCTGCTACTACTACTGTC 232
QY      930 TGTGTTACAACTAGAACAGTTACAGACAGTACCACTGCTGTGTCATCTTTTCAATTCAA 989
Db      233 TACTACTACTGCTACAACTACTCTGCTACTACTACTACTACTACTACTACTACTACTACTAC 292
QY      990 TCCAAGTGTGATAAACAACCAAAACCAATCGAAATTTTGCAACCTATTTCCAACCACTACCAT 1049

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<http://www.genoscope.cns.fr/Tetraodon>.

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ORIGIN

Query Match 6.2%; Score 76.6; DB 9; Length 773;
Best Local Similarity 41.5%; Pred. No. 3.9e-08;
Matches 253; Conservative 31; Mismatches 325; Indels 0; Gaps 0;

618	Qy	TGCTATTGATGCTCAAAATATTCAATATTTGGTATCAAAAAAGGATTAAATGATTGGAATTA	677
161	Db	TGATACTGCTACTACTACWACTGCTACWACTAGTGCWACWACWAGCTACTGCTCWA	220
678	Qy	TCGGTTTCATCTGAATCATTTTAGTTACACTAAAACTTGTACACTCTAATGGAATTCAGAT	737
221	Db	TACTACTAGTGTACTACTGCTACTGCTACTACTGCTACTACTGCTACTACTGCTACT	280
738	Qy	TAAATATCAAAATGTACTCTGCTGTTATCGTCCATTTTATTGATGCTTTATTTTGTCTAC	797
281	Db	TGCTACTACWACTGCWACTACTGCWACTGCTACTACTCTCWA	340
798	Qy	AGATGTTAACCAATATATCTTTTACGATATACCAATGATTATATCTTGTGCTGGCAGTCGCT	857
341	Db	TACTACTACTTCTACTACTACTGCAWACCAGCATACATACTACTGCTACTACTACATGCT	400
858	Qy	GCAAAATAAACCTTTTCACTTTTAAGATGGACTGGATACAAGAAATAGTATGCGCGATCTAA	917
401	Db	ACATACTGCAACTACWCACTGCWACTRCTCTACAGWACTACTACCAWCAACAACACTAC	460
918	Qy	CGGTATTGTCATTTGCTCAACTAGAACAGTTACAGACGATACCACTGCTGTCTACTAC	977
461	Db	WRWCAWRCAACTACTGCTCAACTACTCTCWA	520
978	Qy	TTTACCATTCAAATCCAAAGTGTGATAAAACCAAAACAATCGAAATTTTGCAACCTATTCC	1037
521	Db	TRCTACTACTACTACTACWCTACWACTACWCTACTCTGCTACTCTCAACTGCTACTAC	580
1038	Qy	AACCACTACCATCACAACTTCATATGTTGGTGTGACTTCTTCCTATCTGACTAAGACTGC	1097
581	Db	WACTGCTACWACTGCWACTGCTCAACTACAACACTACTCTCAACTCTCATACTACTACT	640
1098	Qy	ACCAATTTGGTGAACAGCTACTGTTATTTGTATGTTGCCATATCATACTACTACCAACTGT	1157
641	Db	ACTACAACATACACTGCTACTGCTACTACTGCTACTACTGCTACTCTACTCTACTCTC	700
1158	Qy	TACCAGTGAATGGACAGAGAAACAATCACTACCAACAACCTCGTACCAATCCAATGATTC	1217
701	Db	TACTACTACTACTGCTACTACTGCTACTGCTACTGCTACTGCTACTACTCTACTCTACTAC	760
1218	Qy	ARTTGACAC	1226
761	Db	TACTGCTAC	769

RESULT 12	BZ643398	LOCUS	DEFINITION	BZ643398	480 bp	DNA	linear	GSS 29-JAN-2003
				CGA0857C	ZM 0.7 1.5 KB	zea mays genomic clone ZMMBMa011J17,		
						genomic survey sequence.		

ACCESSION	SEQUENCE	ORGANISM
B2643398	GI:28104877	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD
B2643398.1		Clade: Panicoideae; Andropogoneae; Zea
KEYWORDS		
SOURCE		
		Zea mays
		Zea mays

REFERENCE AUTHORS

TITLE	JOURNAL	COMMENT
-------	---------	---------

1 (bases 1 to 480)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGAOW57TM
Contact: Cathy Whitelaw

CONTACT: CARMY MAXIMIAN
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843
Fax: 301-838-0208
Email: white@tigr.org
Seq primer: TF
Class: sheared ends.

Страна: Беларусь

source

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/organism="Zea mays"
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methylation filtered and
sequenced"

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Best Local Similarity 47.6%; Pred. No. 5.6e-08;
Matches 224; Conservative 0; Mismatches 247; Indels 0; Caps 0;
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[illegible]

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DEFINITION	BH355163				
ACCESSION	CH230-81P6.TJ CHORI-230 Segment 1	DNA	694 bp	linear	GSS 03-DEC-2001
VERSION	BH355163				
KEYWORDS	BH355163.1 GI:17285897				
SOURCE	Rattus norvegicus (Norway rat)				

Result No.	Score	Query Match	Length	DB ID	Description
1	1245	100.0	3786	15	US-10-245-802-7
2	1046.6	84.1	3813	15	US-10-245-802-15
3	949	76.2	4383	15	US-10-245-802-21
4	947.4	76.1	3360	15	US-10-245-802-11
5	895	71.9	1404	15	US-10-245-802-9
6	733.4	58.9	1407	15	US-10-245-802-13
7	713.8	57.3	1404	15	US-10-245-802-23
8	574.6	46.2	4332	15	US-10-245-802-17
9	333.6	31.6	6897	15	US-10-245-802-19
10	55.4	4.4	436	9	US-09-864-761-2885
11	53.2	4.4	3111	17	US-10-282-122A-27975
C					Sequence 27975, A


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Db      1948 ACTAATCCCACTGACTCAATAGACACTGTTCATTGTACAAGTTCCA 1992
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RESULT 4
US-10-245-802-11
; Sequence 11, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11
; LENGTH: 3360
; TYPE: DNA
; ORGANISM: Candida albicans
; US-10-245-802-11

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Query Match	76.1%	Score 947.4	DB 15	Length 3360
Best Local Similarity	85.1%	Pred. NO. 9.2e-205		
Matches 1059	Conservative	0	Mismatches 186	Indels 0
				Gaps 0

Qy	1	AAGACAATCACTGCTGTTTTTGGAFAGTTTTAAATTCATTAACCTGGTCCAATGCTGCTAAT	60
Db	52	AAGACAATCACTGCTGTTTTTCAACAGATTTTAAATTCATTTGACTTGGTCTAAATGCTGCTACT	111
Qy	61	TATGCTTTCAAAGGGCCAGGATACCCAACTTGGGAATCGTTTTTGGGTTGGTCTCTTAGAT	120
Db	112	TATAAATATTAAGGACACAGGAACCCCAACTTGGGAATGCTGTTTTTGGGTTGGTCTTTAGAT	171
Qy	121	GGTACCAGTGCCAATCCAGGGGATACATTTCACTTGAATATGCCATGTGTCTTTAAATAT	180
Db	172	GGTACTAGTCAAGTCGCGGAGATACATTTCACTTGAATATGCCATGTGTCTTTAAATTT	231
Qy	181	ACTACTTCAAAAACATCTGTTTGATTTAACTGCGGATGSGTGTAAATATGCTACTTGTCAA	240
Db	232	ACTACTTCTCAAAACATCTGTTTGATTTGACTGCTCATGGTGTTAAATATGCTACATGTCAA	291
Qy	241	TTTTTATTCGTGTGAAGAAATTCACAACTTTTTTCTACATTAACAATGTACTGTGAAACGACGCT	300
Db	292	TTTCAGGCGAGTGAAGAATTTTATGACCTTTTCTACATTAACAATGTACTGTGAGCAATACT	351
Qy	301	TTGAAATCATCCATTAAGGCAATTTGGTACAGTTACTTTTACCAATTTGCATTTCAATTTGGT	360
Db	352	TTGACTCCATCTATTAAAGGCTTTGGGTACTGTCACTTTACCACITTGCAATTCAAATGAGGT	411
Qy	361	GGACAGGTTTCATCAACTGATTTGGAGAGATTCATAAAGTTTTTCTGCTGGTACCAATACA	420
Db	412	GGAACTGGTCTTCTGTTTGATTTGGAGAATTCATAAAGTTTTTACTGCTGGTACTAACACA	471
Qy	421	GTCACTTTAATGATGGTGTATAAAGATATCTCAATTTGATTTGGATTTTGAAGGTCACAC	480
Db	472	GTTACATTTAATGATGGTGGCAAGAAATCTCTATTATGTTGATTTTGAAGGTCACAAAT	531
Qy	481	GTTGATCCAAAGTGCAATATTTGTAATGCTTCCAGAGTTATGGCCAGTCTCCAATTAAGGTACA	540
Db	532	GTCGATCCAAAAGGGTACTTTAACTGATTTCCAGAGTTATACCAAGTCTCAACAAAGGTGCA	591
Qy	541	ACTCTTTTTTGGGCAACCAATGTCAAAATGGTTACACATCTGGTACAAATGGGGTTCTCC	600
Db	592	ACTCTTTTTTGTGCACCAAAATGTGCAAAATGGTTACACATCTGGTACAAATGGGATTCGCT	651
Qy	601	AGTAGTAAACGGTGAAGTTGCTATTGATTTGCTCAAAATATTCATATTTGGTATCAAAAAGGA	660
Db	652	AACACTTATGTGTGATGTTTCAAAATGCAATGCACTGTTTCAAAATATTCATGTTGGTATTCAAAAGGA	711

RESIST 5

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US10-245-802-9
US-10-245-802-9
; Sequence 9, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-9

```

	Query Match	71.9%;	Score 895;	DB 15;	Length 1404;
	Best Local Similarity	83.2%;	Pred. No. 4.9e-193;		
	Matches 1031;	Conservative	0;	Mismatches 205;	Indels 3; Gaps 1;
Qy	7	ATCACTGGTGTGTTTTGATAGCTTTTAATTCATTAACCTTGGTCCAAAGCTGCTAAATATGCT	66		
Db	58	ATTACGGGTGTTTTCAATAGCTTTTGGATTGGTTGATGGAACAAGAGCTGGTAAATATGCT	117		
Qy	67	TTCAAAAGGGCCAGGATACCCAACTTGGAAATGCTGTTTTGGGTGGTCTCTTAGATGGTACC	126		
Db	118	TATTAAGGGCCCAATATAGACCAACTTGGAAATGCTGTTTTGGGTGGTCTCTTAGATGGTACT	177		

127 AGTCCCAATCCAGGGATACATTCACATTTGAATATGCAATGCTGTGTTTAAATATCTACT 186
178 AGTGCAATCCAGGAGACACATTCACATTTGAATATGCAATGCTGTGTTTAAATATCTACT 237
187 TCACAAACATCTGTTGATTTAACTGCGGATGGTGTAAATATGCTACTTGTCAATTTTAT 246
238 GATCAAAACATCTGTTGATTTAACTGCGGATGGTGTAAATATGCTACTTGTCAATTTTAT 297
247 TCTGGTGAAGAAATTCACAACTTTTCTACATTTAATGCTACTGTCGACGCTTTGAA 306
298 TCAGGTGAAGAAATTTACAACTTTTCTACATTTAATGCTACTGTCGACGCTTTGAA 357
307 TCATCCATTAAGGCAATTTGGTACAGTTTCTTACCAATTTGATTTGATTTGTTGGAACA 366
358 TCATCTATTAAAGCTTTGGGTACAGTTTCTTACCAATTTGATTTGATTTGTTGGAACA 417
367 GGTTCATCAACTGATTTGGTGAAGATTTCTAAATGTTTAACTGCTGGTACCAATPACAGTCA 426
418 GGTTCATCGTGTGATTTGGTGAAGATTTCTCAATGTTTAAAGCTGGCACCACACAGTTTACT 477
427 TTTAATGATGCTGAATAAGATATCTCAATTTGATTTGATTTGATTTGATTTGATTTGAT 486
478 TTTAATGATGCTGAATAAGATATCTCAATTTGATTTGATTTGATTTGATTTGATTTGAT 537
487 CCAAGTGCATATTTGATGCTTTCCAGAGTTATGCCAGTCTCAATTAAGGTCACAACTCTT 546
538 GCAAGTGCATATTTGATGCTTTCCAGAGTTATGCCAGTCTCAATTAAGGTCACAACTCTT 597
547 TTTTGGGACCAACAATGTTGAAGATTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGAT 606
598 TATGTTGGGACCAACAATGTTGAAGATTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGAT 657
607 AACGGTGAAGTGTGATTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGAT 666
658 ACTGGTGAAGTGTGATTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGAT 717
667 GATTTGGAATATCCGGTGTGATTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGATGCTTT 726
718 GATTTGGAATATCCGGTGTGATTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGATGCTTT 777
727 GGAATTCAGATTAATCAAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 786
778 GGTATTTCTACACATATGAAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 837
787 ATTTCTGCTACAGATGTTAAACCAATATCTTTAGCATATATCAATGATTTATCTTGCT 846
838 ACTCTGGTGTGAGGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 894
847 GGCAGTCTGCTGCAAGTAAACCTTTTCACTTTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
895 GGTAGTTCCTTACAAAGTAAAGCGGTTTCAATTTAAGTGTGAGGAGATACAAATATAGTGA 954
907 GCGGATCTAACCGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 966
955 GCTAATTTCTAACCGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 1014
967 GCTGCTACATCTTTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1026
1015 GCTGCTACATCTTTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1074
1027 CAACCTATTCACCACTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1086
1075 CAACCTATTCACCACTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1134
1087 ACTAAGATGCTACCACTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1146
1135 ACTAAGATGCTACCACTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1194
1147 ACCCAACTGTTTACCACTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1206
1195 ACCCAACTGTTTACCACTTACCAATCAATCCAAAGTGTGATTAACCAAAACCAATGAAATTTTG 1254

1207 CCAACTGATTTCAATTTGACACAGTGGTGGTACAAAGTTCCA 1245
1255 CCAACTGATTTCAATTTGACACAGTGGTGGTACAAAGTTCCA 1293

RESULT 6
US-10-245-802-13
; Sequence 13, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; FILE REFERENCE: 013361.4003
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US/10/245,802
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1407
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-13

Query Match 58.9%; Score 733.4; DB 15; Length 1407;
Best Local Similarity 74.5%; Pred. No. 2.6e-156;
Matches 923; Conservative 0; Mismatches 316; Indels 0; Gaps 0;

7 ATCACTCGTGTGTTTGTAGTATTTTAAATTCATTTAACTTTGGTCCAAATGCTTAATATGCT 66
58 ATTACAGTGTGTTTCAATAGTATTTTAAATTCGTTAACTTTGGGCCAATGCTGCTTCTTATCCA 117
67 TTCAAAGGCCAGGATACCCAACTTGAATGCTGTTTGGGTGGTCTTATAGATGCTTACC 126
118 TATAGAGGTCGAGCTACTCTTACTTGGACCGCTTAATAGATGGTCTTTATAGATGAGCT 177
127 AGTGCCCAATCCAGGGGATACATTCACATTTGAATATGCAATGCTGTGTTTAAATATATACTACT 186
178 ACTGCTAGTGTGTTGATGACATTCACATTCGTTAGACATGCTGTTGTTTCAATTTATTA 237
187 TCACAAACATCTGTTGATTTTAACTGCGGATGGTGTAAATATGCTACTTGTCAATTTTAT 246
238 GATCAAAAGCTCAATTTGATTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
247 TCTGGTGAAGAAATTCACAACTTTTCTACATTTAATGCTACTGCTGTAACAGCGCTTTGAA 306
298 TCTGCCGAAGAGTTTACTACTTTTCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
307 TCATCCCAATTAAGGCAATTTGGTACAGTTTACTTTTACCAATTTGATTTCAATTTGTTGGAACA 366
358 GCTGACACCAAGCCATAGGAACTGTAACTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
367 GGTTCATCAACTGATTTTGGGAGATTTCTAAATGTTTAACTGCTGCTGTAACCAATPACAGTCA 426
418 GGTTCAGATGTTGATTTGGGCAAAATTCCTCAATGTTTAACTGCTGCTGTAACCAATPACAGTCA 477
427 TTTAATGATGCTGAATAAGATATCTCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 486
478 TTTAATGATGCTGAATAAGATATCTCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 537
487 CCAAGTGCATATTTGATGCTTTCCAGAGTTATGCCAGTCTCAATTAAGGTCACAACTCTT 546
538 TCCAGCGATGCTATCTTGTGCTCAAGAAATTTTACCGAGTCTTTCACAGCGATTAATCTT 597
547 TTTTGGGACCAACAATGTTGAAGATTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGATGCT 606
598 TTTTCTTCCCAAGAAATGTCGCAATGTTTATCTTCTGCTGTAACATGCGGATTTTTCGAGTCT 657
607 AACGGTGAAGTGTGATTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGATGCTTTGATGCT 666
658 GGTACTGCTGCTACTATAGATTTGTTTCCACAGTTCATGTCGGGATATCAATTTGGGTTGAT 717

Qy	1201	ACCAATCCAACTGATTCAATTTGACACAGCTGGTGGTACAAGTTTCCA	1245
Db	1249	ACTAATCCCACTGGTTTCATAGACACTGTTATGTGCAAAATTTCCA	1293

Db 115 GCTCGATACGAAGAAATATCTACTCTTTACCGCTAAATGCTCAATGGAAATGGGCTTTGGAT 174
Qy 121 GGTACAGTCCCAATCCAGGGGATACATTCACATGGAATATGCAATGCGATGTTTAAATAT 180
Db 175 GGTACTATTGCCAGTCCGGGTGATACATTTACATTTAGTCATGCGCTGTGTATATAATTC 234
Qy 181 ACTACTTTCAAAAATCTGTGTGATTTAACTGCCGATGGTGTAAATATGCTACTTTGTCAA 240
Db 235 ATGAGCTAGCAAACTCAGTGCATTAACCTGCACTCTATTGCATATGCCATGTGAC 294
Qy 241 TTTTATTCTGGTGAAGAAATCAAACTTTTTCATATTAACATGATCTGTGAACGAGCT 300
Db 295 TTTGATGCTGTGGAAGACACTAAAGTTTTCAGATTTGAAGTGTACGGTGAATGATGAG 354
Qy 301 TTGAATCATCCATTAGGCATTTGGTGTACAGTTACTTTTACCAATGCTCAATGTTGGT 360
Db 355 TTGACGAAGATACCAAGCTTTTGGAAAGTGTATTATTGCTTATGCTTTCAATGTTGGA 414
Qy 361 GGACACAGTTCATCAACTGATTTGGAAGATTTCTAAATGTTTAACTGCTGCTGTACCAATACA 420
Db 415 GGTTCGGATCTAAATCTACGATTAACAGACTCCAAATGTTTTCAGTGGGTACAACT 474
Qy 421 GTCAATTTAATGATGTGATTAAGATATCTCAATGATGTTGAGTTTGAAGTCAACC 480
Db 475 GTCAAGTTTGTGACGGAACCAATCAACTTCTACAACTTCTCAAAATTTTCTTCCCGAAGA 534
Qy 481 GTTGATCCAAGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAGGTCA 540
Db 535 GAACTAGCGTTGGTCTAGTTGTTAGTCAAGACTTTCCATGTCGCTCGATACAATGACT 594
Qy 541 ACTCTTTTGTGGCACCACCAATGTGAATGTTTACACATCTGTGTCAATGGGTTCTCC 600
Db 595 AATTTTGTATGCTACACCTGTTTTCATGGTTATCAGCTGGGTAGTTAGTTTACA 654
Qy 601 AGTAGTAACCGTGAAGTGTGATGTTGATGTTCAATATTCATATGTTGTATCAAAAAGGA 660
Db 655 TCTAATGATGATGATTTTGAATTTGATTTCTTCTATACATGTTGTGTATAAATCAATGAA 714
Qy 661 TTAATGATGGAATTTCCGTTTTCATCTGAAATCAATTTAGTTTACACTAAACTGTGACA 720
Db 715 ATAATGATGAGTATGCCAGTATCTCTGTTCCCTTCGATCATATCTAAGATGACA 774
Qy 721 TCTAATGGAATTCAGATTAATATCAAAATGTACTGCTGTTATCTGCTCAATTTATGAT 780
Db 775 TCAGTGCACCTTTACATTTAGTTTAAACAAATCTCTGAGTTATCGACCTTTGTGAT 834
Qy 781 GCTTATATTTCTGCTACAGATGTTTAAACAAATATCTTTAGCATATACCAATGATTAAT 840
Db 835 GCGATTGTTCAAAATACCAACGACAGAACCTTTTGTGTAATAATATACCAATGATGTC 894
Qy 841 TGTCTGGCAGTCTGTGCAAGGTAAACCTTTAC ---TTTAAAGTGCATGGATACAAG 897
Db 895 TGTGTGAATGGCATATACAGTCCATACCTTTTCAAGTTTCTTTCTCAGCCCAATTTTA 954
Qy 898 AATAGTGAATGCGGATCTAACCGTATTTGTCATTTGCTGCTCAACTAGAACAGTTTACAGAC 957
Db 955 TATCAGCGGCTTTAGCTATTTGGTGCAGACTAGTTGTACCAATCCACAGTATAGGT 1014
Qy 958 AGTACCACTGCTGCTACATCTTTTACCAATTCATCCAAAGTGTGTATATAAACCACCAATC 1017
Db 1015 TCCATTACCAAGATACCAATTAACCTTTCAATTTCCCGACTCCAGAAAACCAAAACAATT 1074
Qy 1018 GAATTTTGCACCTTTTCCAAACCACTACCATCAACTTCATATGTTGTGTGACTACT 1077
Db 1075 CTAGTCTTAGAGCCCATACCCACCACTACGGTAAACAATTCACACCAATGGCTTTGATACT 1134
Qy 1078 TCCTATCTGATAAGACTGCAACCAATTTGGTGAACAGCTACTGTTTATTTGATGTGCCA 1137
Db 1135 TGGTATATTAATAAGAAAGCCCAATTTGGTGCACAGCTACTGTTTTCATTTGATTTCCA 1194
Qy 1138 TATCATACTACCAACTGTTTACAGTGAATGGACAGGAACATTCATCACTACCAACAAT 1197

Db 1195 CAACATACAGCTACTTTTGACCAATATTTGCCAAGAAATCAAGTACGCGCAACCACT 1254
Qy 1198 CGTACCACATCCAACTGATTCATTCACACAGTGGTGGTACAAAGTTTCCA 1245
Db 1255 TACTTCGATGACATAGACTTGGTGCATCTGTTCATTTGTGAAAATTTCCA 1302
RESULT 10
US-09-864-761-2885
; Sequence 2885, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2885
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000018.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1

US-09-864-761-2885

	Query Match	4.4%; Score 55.4; DB 9; Length 436;
	Best Local Similarity	48.6%; Pred. No. 0.019;
	Matches 152; Conservative 0;	Mismatches 161; Indels 0; Gaps 0;
Qy	914	CTAAGCGTATTGTCATTTGCTTGTCTACAACAGTTTACAGACAGTACCACTGCTGTC
Db	68	CTATTGTCACCTAATTACCACTACCACTTGTACTACCACTATCATCTACTACCATCA
Qy	974	CTACTTTTACCAATTCCAATCCAAAGTTTGATAAAACCAAAACAAATCGAAATTTGCAACCTA
Db	128	CTACTAATACTATCATTTACCACTACTATTACCAITTCACGACTATCATCTACTACTACTA
Qy	1034	TTCCGAACCACTACCATCAGAACTTCATATGTTGGTGTGACTACTTTCCTATCTGACTAAGA
Db	188	CCACCTCCCACTTACTACTACTAATGCTATCATTTACTACTGCTTCTATAATTAATCTA
Qy	1094	CTGCACCAATTTGGTGAACAGCTACTGTTATTTGTTGATGTGCCATATCATACTACCACTA
Db	248	CTCTCTATCTCCTACCAATTACTACTACTAGTAGTATCACCATTTACTACTACTACTATCA
Qy	1154	CTGTTTCCAGTGAATGGACAGGAAACAATCACTACCAACCAAACTCGTACCAATCCAACTG
Db	308	CTATTACCAACCACTTACTACTATCATTTACTACTACTACTACCAACCACTACTACTACTG
Qy	1214	ATTCAATTGACAC
Db	368	CTGTCAATTACTAC

RESULT 11
US-10-282-122A-27975/c
Sequence 27975, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308

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; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
;
; NUMBER OF SEQ ID NOS: 78614
;
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27975
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: Mycoplasma pneumoniae
US-10-282-122A-27975

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Query Match	4.3%;	Score 53.2;	DB 17;	Length 3111;
Best Local Similarity	47.8%;	Pred. No. 0.16;		
Matches 154;	Conservative 0;	Mismatches 168;	Indels 0;	Gaps 0;
Qy	169	GTGTTTAAATATACTACTTCACAAACATCTGTTGATTAACTGCCGATGGTGTAAATAT	228	
Db	1892	GTTTTCAATAGCTGGTTCGACTGCACACGCTGTTTGACTCTTGTTCAACTGGGCTCTTCA	1833	
Qy	229	GCTACTTGTCAATTTTATTCTGGTGAAGAATTCACAACTTTTCTTCAATTAACATGTA	288	
Db	1832	ACGGTCTCTGCACATAATGTTGTTGAAAGTTTCAACAATGGTTCACAGCAAGTGGTG	1773	
Qy	289	GTGAACAGCGCTTTGAAATCAATCATTAAGGCAITTTGGTACAGTACTTTACCAATGCA	348	
Db	1772	TCTTCAACAACTGCTAATACTTCTTGTTCTACTGCTTTCTCAGTAACGTGAACAGTTCA	1713	
Qy	349	TTCAATGTTGGTGGACACAGGTTTCATCAACTGATTTTGGAGATTCATAATGTTTTACTG	408	
Db	1712	GTAAACAACCTGGTGCTGTTTCTAGTTGAACAGTTTCAACGGGTTCTAAACTTACTGGT	1653	
Qy	409	GGTACCAATACAGTCACTTAATATGATGGTGTGATAAAGATATCTCAATGATGTGAGTT	468	
Db	1652	TCTGTAAAGTTCAACCGTTTCAACAACCTGGAGTTGATGACAACTAGGTTCAATTTG	1593	
Qy	469	GAAGAAGTCAACCGTTGATCCAA	490	
Db	1592	GCACTTACACAGTTGATTCAA	1571	

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RESULT 12
US-10-311-455-1075/c
; Sequence 1075, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Imm
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1075
; LENGTH: 7758
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1075

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Query Match	4.0%	Score 49.4	DB 15	Length 7758
Best Local Similarity	47.7%	Pred. No. 1.8		
Matches 177	Conservative 0	Mismatches 191	Indels 3	Gaps 1
Qy	859	CAAGTAAACCTTTCACCTTTAAGTACCTGGATACAAGATAGTACGATCGCGATCTTAAC	918	

Db 6240 CCAACTACCCCTCCTACTACACCAATACTTCAACTACCCCTCCTACTACACCAATACT 6181
Qy 919 GGTATTGTCATTGTTGCTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCACTACT 978
Db 6180 TCAACTACCCCTCCTCCTCCTCCAAATCTTTAACTACCCCTACTACTCTCTAACTACT 6121
Qy 979 TTACCATTCATCCAACTGTTGATATAAACCAAAACAAATCGAAATTTTGGCAACTATTCCA 1038
Db 6120 TCAACTACAAACCTACTACTCTTAAAAACCCCACTACCCCTTCTTAATATCTCCAAATACT 6061
Qy 1039 ACACCTACCATCAAACTTCATATGTTGGTGTGACTACTTCCCTATCTGACTAGACTGCA 1098
Db 6060 CCAACTACCCCTCCTACTACTTCCAAATCTTCAACTACCCCTCCTACTCTCCAACTACT 6001
Qy 1099 CCAATTGGTGAACAGCTACTGTTATTGTTGATGTGCAATATCATATACCAAACTGTT 1158
Db 6000 CCAATTACCCCTCCTACTACTTCCAAATCTTAACTACCCCTCCTACTACTTCCAAATACT 5941
Qy 1159 ACCAGTGA---ATGACAGGAACAAATCACTACCAACCAAACTGCTGTAACCAATCCAACTGAT 1215
Db 5940 TCAACTACCCCATCTACTACTCTTAAAAACTCTAACTACTTCTCCTACTAATCCAAATACT 5881
Qy 1216 TCAATTGACAC 1226
Db 5880 TCAACTACCCCT 5870

RESULT 13

US-09-968-007A-427
; Sequence 427, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 427
; LENGTH: 267156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-427

Query Match 3.9%; Score 48.8; DB 11; Length 267156;
Best Local Similarity 46.2%; Pred. No. 14;
Matches 241; Conservative 0; Mismatches 272; Indels 9; Gaps 2;
Qy 704 ACACATAAACTTGACATCTAATGGAATTCAGATTAAATATCAAAATGTACCTGCTGGTT 763
Db 12574 ATACTACCACTGGCACTACTGATGATCTGTTCTATACACCAACATCTTCCCAAGTACTA 12633
Qy 764 ATCGTCCATTTATTGCTTTATATTTCTGTACAGATGTTAAACATATATCTTTAGCAT 823
Db 12634 CTAGTGTACAACTAACTACTACTGTTCTGTATACAACTTCT---CCTTCCCTACAACTA 12690
Qy 824 ATACCAATGATTATATGCTTGGCAGTGTCTGCAAGTAAACCTTTTCACTTTAGAT 883
Db 12691 CTACTAATGCTAGCACTAATGCTACTGTTCCTATCACAAACCACTTTTCCCAACAAGTA 12750

Qy 884 GGACTCGATACAGAATACTGATGCGGATCTAACGGTATTGTTCATTGTTGCTACAACTA 943
Db 12751 CTATTGGTGTGTTCAACTAATGCTACTGTTCCCAATAACAACCTGCTTTCCCAACAAATG 12810
Qy 944 GAACAGTTACAGACAGTACCACTGCTG-----TCACTACTTTTACCATTCAATCCAAAGT 997
Db 12811 CTAGTACTGCTAGCACTAATGCTACTGTTCTTATCAACCAACATGTTTTCGAACAAGTA 12870
Qy 998 TTGATAAAAAACCAAAACAAATCGAAATTTTGCACCACTATTCCAAACCACTACCACTCAAACTT 1057
Db 12871 CTATTGGTGTGTTCAACTAATGCTACTGTTCCGATACAACTGCTTTCCCAACAAATA 12930
Qy 1058 CATATGTTGGTGTGACTACTTCTATCTGACTAAGACTGCACCAATTTGGTGAACAGCTA 1117
Db 12931 CTACTACTGCTAGCACTAATGCTACTTATCTCTATCAACCAACCACTTTTTCGAACAAGTA 12990
Qy 1118 CTGTTATTCTTGTGATGCGCATATCATACTACCACTGTTTACCAGTGAATGCACAGGAA 1177
Db 12991 CTATTAGTGTGTTCAACTAGTACTGTTCTGATACAACTGCTCTCTTCCCTTACAAGTA 13050
Qy 1178 CAATCACTACCAACCAACTCGTACCAATCGTACCAATCGAATGATTCAA 1219
Db 13051 CTACTAGTCTAGCACTAATGCTACCCCTGTTCTCTATCAAA 13092

RESULT 14

US-09-263-959-1
; Sequence 1, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy B.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-1

Query Match 3.9%; Score 48.8; DB 9; Length 684973;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 241; Conservative 0; Mismatches 272; Indels 9; Gaps 2;
Qy 704 ACACATAAACTTGACATCTAATGGAATTCAGATTAAATATCAAAATGTACCTGCTGGTT 763

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 09:36:50 ; Search time 179 Seconds
(without alignments)

11380.807 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA.*

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6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225.8	98.5	3573	4	US-09-248-796A-2140
2	1029	82.7	2340	4	US-09-248-796A-2599
3	728.2	58.5	1536	4	US-09-248-796A-22
4	671.6	53.9	3180	4	US-09-248-796A-20
5	574.6	46.2	1941	4	US-09-248-796A-2598
6	509.8	40.9	900	4	US-09-248-796A-2142
7	414.6	33.3	690	4	US-09-248-796A-2595
8	392	31.5	2436	4	US-09-248-796A-2141
9	293.2	23.6	699	4	US-09-248-796A-19
10	253.6	20.4	462	4	US-09-248-796A-16
11	149.8	12.0	294	4	US-09-248-796A-9483
12	82.4	6.6	100	1	US-08-145-705A-32
13	82.4	6.6	100	1	US-08-145-705A-34
14	76	6.1	100	1	US-08-145-705A-33
15	68	5.5	100	1	US-08-145-705A-36
16	61.4	4.9	5511	3	US-08-928-361B-2
17	61.4	4.9	5511	4	US-09-588-995A-2
18	61.4	4.9	7334	3	US-08-928-361B-1
19	61.4	4.9	7334	4	US-09-588-995A-1
20	57.2	4.6	100	1	US-08-145-705A-37
21	57	4.6	100	1	US-08-145-705A-35
22	55.4	4.4	601	4	US-09-949-016-180704
23	55.4	4.4	70770	4	US-09-949-016-16938
24	55.2	4.4	5163	3	US-08-700-651-1
25	55.2	4.4	5163	4	US-08-928-361B-4
26	55.2	4.4	5163	4	US-09-588-995A-4
27	55.2	4.4	5318	3	US-08-700-651-2

28	55.2	4.4	5318	3	US-08-928-361B-3	Sequence 3, Appli
29	55.2	4.4	5318	4	US-09-588-995A-3	Sequence 3, Appli
30	53.6	4.3	528	4	US-09-248-796A-2593	Sequence 2593, Ap
31	53.6	4.3	832	4	US-09-621-976-2813	Sequence 2813, Ap
32	52.8	4.2	1506	4	US-09-248-796A-15	Sequence 15, Appl
33	51.2	4.1	1141	4	US-09-806-708B-22	Sequence 22, Appl
34	50.6	4.0	1671	4	US-09-248-796A-8235	Sequence 8235, Ap
35	50	4.0	1071	1	US-08-357-962-1	Sequence 1, Appli
36	50	4.0	1071	1	US-08-878-106-1	Sequence 1, Appli
37	49.2	4.0	832	4	US-09-621-976-2813	Sequence 2813, Ap
38	48.6	3.9	425	1	US-08-357-962-5	Sequence 5, Appli
39	48.6	3.9	425	1	US-08-878-106-5	Sequence 5, Appli
40	48.6	3.9	1141	4	US-09-806-708B-22	Sequence 22, Appl
41	47.6	3.8	83428	4	US-09-949-016-13610	Sequence 13610, A
42	47	3.8	1158	4	US-09-248-796A-23	Sequence 23, Appl
43	47	3.8	1569	4	US-09-248-796A-18	Sequence 18, Appl
44	46.6	3.7	4184	4	US-09-949-016-4495	Sequence 4495, Ap
45	46.6	3.7	12191	4	US-09-949-016-16237	Sequence 16237, A

ALIGNMENTS

RESULT 1

US-09-248-796A-2140
; Sequence 2140, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2140
; LENGTH: 3573
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2140

Query Match	98.5%	Score	1225.8	DB	4	Length	3573
Best Local Similarity	99.0%	Pred. No.	6.8e-313	Indels	0	Gaps	0
Matches	1233	Conservative	0	Mismatches	12		
Qy	1	AAGACAATCACTGCTGTTTTTGATAGTTTTTAATTCATTAACTTGGTCCAATGCTGCTAAT	60				
Db	58	AAGACAATCACTGCTGTTTTTGATAGTTTTTAATTCATTAACTTGGTCCAATGCTGCTAAT	117				
Qy	61	TATGCTTTCAAAGGGCCAGGATACCCAACTTGGAAATGCTGTTTTGGGTTGGTCTTAGAT	120				
Db	118	TATGCTTTCAAAGGGCCAGGATACCCAACTTGGAAATGCTGTTTTGGGTTGGTCTTAGAT	177				
Qy	121	GGTACCACTGCCATCCAGGGGATACATTCATGTAATGATGCCATGCTGTTTAAATAT	180				
Db	178	GGTACCACTGCCATCCAGGGGATACATTCATGTAATGATGCCATGCTGTTTAAATAT	237				
Qy	181	ACTACTTCACAAAACATCTGTTGATTTAACTCCGATGGTGTAAATATGCTACTTGTCAA	240				
Db	238	ACTACTTCACAAAACATCTGTTGATTTAACTCCGATGGTGTAAATATGCTACTTGTCAA	297				
Qy	241	TTTTATTCTGCTGAAGAAATTCACAACTTTTCTCATTTAAACATGTAATGTAACGACGCT	300				
Db	298	TTTTATTCTGCTGAAGAAATTCACAACTTTTCTCATTTAAACATGTAATGTAACGACGCT	357				
Qy	301	TGAAATCATCCATTAAGGCATTTGGTACAGTATTTTACCAATTCGATTCGATTCGATTCG	360				
Db	358	TGAAATCATCCATTAAGGCATTTGGTACAGTATTTTACCAATTCGATTCGATTCGATTCG	417				

QY 361 GGAACAGGTTTCATCAACTGATTTTGGAGATTCCTAAATGTTTAACTGCTGTGACCAATACA 420
| | | | |
Db 418 GGAACAGGTTTCATCAACTGATTTGGAAGATTCCTAAATGTTTAACTGCTGTGACCAATACA 477
| | | | |
QY 421 GTACATTTAAATGATGGTGAATAAGATATCTCAATTTGATGTTGAGTTTGAAGAGTCAACC 480
| | | | |
Db 478 GTACATTTAAATGATGGTGAATAAGATATCTCAATTTGATGTTGAGTTTGAAGAGTCAACC 537
| | | | |
QY 481 GTTGATCCAAAGTGCATATTTGATGCTCCAGAGTTATGCAAGTCTCAATAGGTCACA 540
| | | | |
Db 538 GTTGATCCAAAGTGCATATTTGATGCTCCAGAGTTATGCAAGTCTCAATAGGTCACA 597
| | | | |
QY 541 ACTCTTTTGTGGCACCACCAATGTGAAATGGTTACACATCTGGTCAATGGGGTCTCC 600
| | | | |
Db 598 ACTCTTTTGTGGCACCACCAATGTGAAATGGTTACACATCTGGTCAATGGGGTCTCC 657
| | | | |
QY 601 AGTAGTAACGGTGAACGTTGCTATTTGATGCTCAATATTCATATTTGGTATCACAAGGA 660
| | | | |
Db 658 AGTAGTAACGGTGAACGTTGCTATTTGATGCTCAATATTCATATTTGGTATCACAAGGA 717
| | | | |
QY 661 TTAATGATTTGGAATATTCGGTTTCATCTGAATCATTTAGTTACACTMAAACTGTGACA 720
| | | | |
Db 718 TTAATGATTTGGAATATTCGGTTTCATCTGAATCATTTAGTTACACTMAAACTGTGACA 777
| | | | |
QY 721 TCTAATGGAATTCAGATTTAAATATCAAAATGTACCTGCTGGTTATCGTCCATTTATGAT 780
| | | | |
Db 778 TCTAATGGAATTCAGATTTAAATATCAAAATGTACCTGCTGGTTATCGTCCATTTATGAT 837
| | | | |
QY 781 GCTTATATTTCTGTACAGATTTAACCAATATATCTTTAGCATATACCAATGATTATACT 840
| | | | |
Db 838 GCTTATATTTCTGTACAGATTTAACCAATATATCTTTAGCATATACCAATGATTATACT 897
| | | | |
QY 841 TGTGCTGGCAGTCTGTGCAAGTAAACCTTTCACTTTAAGATGGACTGCATCAAGAAT 900
| | | | |
Db 898 TGTGCTGGCAGTCTGTGCAAGTAAACCTTTCACTTTAAGATGGACTGCATCAAGAAT 957
| | | | |
QY 901 AGTGATCCGGATCTAACGGTATTTGTCATTTGTTGCTACAACTAGAACAGTTACAGACGT 960
| | | | |
Db 958 AGTGATCCGGATCTAACGGTATTTGTCATTTGTTGCTACAACTAGAACAGTTACAGACGT 1017
| | | | |
QY 961 ACCTGCTGTCACTACTTTACCATTAATCCAAAGTTGATTAACCAAAACCAATCGAA 1020
| | | | |
Db 1018 ACCACTGCTCACTACTTTACCATTAATCCAAAGTTGATTAACCAAAACCAATCGAA 1077
| | | | |
QY 1021 ATTTTGCAACCTATTCCAAACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCC 1080
| | | | |
Db 1078 ATTTTGCAACCTATTCCAAACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCC 1137
| | | | |
QY 1081 TATCTGACTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATTTGTTGATGGCCATAT 1140
| | | | |
Db 1138 TATCTGACTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATTTGTTGATGGCCATAT 1197
| | | | |
QY 1141 CATACTACCAACTGTTTACAGTGAATGGACAGGAACATCACTACCAACCAACTCGT 1200
| | | | |
Db 1198 CATACTACCAACTGTTTACAGTGAATGGACAGGAACATCACTACCAACCAACTCGT 1257
| | | | |
QY 1201 ACCAATCCACTGATTCATTTGACACAGTGTGTGTGACAGTTCCA 1245
| | | | |
Db 1258 ACCAATCCACTGATTCATTTGACAGTGTGTGTGCAAGTTCCA 1302
| | | | |

RESULT 2
US-09-248-796A-2599
; Sequence 2599, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2599
; LENGTH: 2340
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1478)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-248-796A-2599

Query Match 82.7%; Score 1029; DB 4; Length 2340;
Best Local Similarity 89.2%; Pred. No. 4.2e-261;
Matches 1110; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 1 AAGACATCAGTCGGTGTGTTTTCATAGTTTAAATTCATTAACCTGGTCCAAATGCTGCTAAT 60
| | | | |
Db 58 AAGGCGATCAGTCGGTATTTTCAATAGTATGACTCATTAACCTGGTCCAAATGCTGCAAT 117
| | | | |
QY 61 TATGCTTTCAAAGGCGCAGGATACCCAACTTGGAAATGCTGTTTGGGTTGGTCTTAGAT 120
| | | | |
Db 118 TAGGCTTTCAAAGGACGAGATACCCAACTTGGAAATGCTGTTGTTGGTGGTTCATAGAT 177
| | | | |
QY 121 GGTACAGTGCCTAATCCAGGGGATACATTCACATTTGAATATGCCATGTGTGTTAAATAT 180
| | | | |
Db 178 GGTACAGTGCCTAATCCAGGGGATACATTCATATTTAAACATGCCATGTGTGTTAAATTC 237
| | | | |
QY 181 ACTACTTCAAAACATCTGTTGATTTAACTGCGGATGTTGTTAAATATGCTACTTGTCAA 240
| | | | |
Db 238 ACTGCTTCCAAAAATCTGTTGATTTGACTGCGGATGTTGTTAAATATGCTACTTGTCAA 297
| | | | |
QY 241 TTTTATTTCTGGTGAAGATTCACAACTTTTCTACATTAACATGCTGTGAACGACGCT 300
| | | | |
Db 298 TTTTATTTCTGGTGAAGATTTACAACTTTTCTTCAATTAATGTACAGTGAACAATAT 357
| | | | |
QY 301 TTGAATATCATTCATTAAGGCATTTGGTACAGTTACTTTTACCAATTTGCAATTCATGTTGGT 360
| | | | |
Db 358 TTGAGATCATCTATTAAAGGCTTTGGGTACGGTTACTTTTACCAATTTGCAATTCATGTTGGT 417
| | | | |
QY 361 GGAACAGGTTTCATCAACTGATTTGGAAGATTCCTAAATGTTTAACTGCTGTGACCAATACA 420
| | | | |
Db 418 GGAACAGGTTTCATCACTGTTGGAAGATTCCTAAATGTTTAACTGCTGTGACCAATACG 477
| | | | |
QY 421 GTACATTTAAATGATGGTGAATAAGATATCTCAATTTGATGTTGAGTTTGAAGAGTCAACC 480
| | | | |
Db 478 GTACATTTAAATGATGGCAGTGAATAAGCTCTCAATGCTGTTAAATTTGGAAGAGTCAACA 537
| | | | |
QY 481 GTTGATCCAAAGTGCATATTTGATGCTCCAGAGTTATGCCAAGTCTCAATAGGTCACA 540
| | | | |
Db 538 GTTGATCCAAAGTGGGTATTTGACTACTTCCAGATTTATGCCAGTCTCAATAAAATGCT 597
| | | | |
QY 541 ACTCTTTTGTGGCACCACCAATGTGAAATGGTTACACATCTGGTACATGGGTTCTCC 600
| | | | |
Db 598 ACTCTTTTGTGGCACCACCAATGTGAAACGGTTACACATCTGGTCAATGGGATTTCTCC 657
| | | | |
QY 601 AGTAGTAACGGTGAACGTTGCTATTTGATGCTCAAAATTTCAATTTGATATTCACAAAGGA 660
| | | | |
Db 658 ACTAGTTATGGGATGTTGCTATTTGACTGTTCAATGTACATATTTGTTTCAAAAGGA 717
| | | | |
QY 661 TTAATGATTTGGAATTTATCCGGTTTCATCTGAATCATTTAGTTTACACTMAAACTGTGACA 720
| | | | |
Db 718 GTAAATGATTTGGAATCATCCAGTTACGTCCTGAATCATTTAGTTTACACTMAAAAGCTGTCA 777
| | | | |
QY 721 TCTAATGGAATTCAGATTTAAATATCAAAATGCTGCTGGTATCGTCCATTTATGAT 780
| | | | |
Db 778 TCTTTTGGTATCTCTATCAATCAAAATGTTTCTCGCGGTTTATCGTCAATTTATGAC 837
| | | | |
QY 781 GCTTATATTTCTGTACAGATTTAACCAATATATCTTTAGCATATACCAATGATTATACT 840
| | | | |
Db 838 GCTTATATTTCTCCCTCAGATTAACCAATATACCAATTTGCTGTTAATAAATGACTATACT 897
| | | | |

841 TGTGCTGGCAGTCTCTGCAAGATAAACCTTTTCACTTTTAAGATGGAAGTGGATCAAGAAAT 900
898 TGTGTTGATGATTAATGGCAACATGCACTTTTCACTTTTAAGATGGAAGTGGATTAAGAAAT 957
901 AGTATGCGCGGATCTAAGCGGTATTGTGCTCAATTTGCTCAAACTAGAACAGTTTACAGACAGT 960
958 AGTATGCGCGGATCTAAGCGGTATTGTGCTCAATTTGCTCAAACTAGAACAGTTTACAGACAGT 1017
961 ACCACTGCTGTCACCTTTTACCAATTCATTCAGAGTGTGATTAACCAAAACCAATCGAA 1020
1018 ACCACTGCTGTCACCTTTTACCAATTCATTCAGAGTGTGATTAACCAAAACCAATCGAA 1077
1021 ATTTTGAACCTTATTCGAACCTTACCAATTCATTCAGAGTGTGATTAACCAAAACCAATCGAA 1080
1078 ATTTTGAACCTTATTCGAACCTTACCAATTCATTCAGAGTGTGATTAACCAAAACCAATCGAA 1137
1081 TATCTGACTAGAGTCTGCAACCAATTTGGTGAACAGCTACTGTTATTTGATGTCCTCATAT 1140
1138 TATCTGACTAGAGTCTGCAACCAATTTGGTGAACAGCTACTGTTATTTGATGTCCTCATAT 1197
1141 CATCTACCAACCTGTTTACAGAGTGAATGGACAGAACCAATCTACTACCAACCAACTCGT 1200
1198 CATCTACCAACCTGTTTACAGAGTGAATGGACAGAACCAATCTACTACCAACCAACTCGT 1257
1201 ACCAATCCAACCTGTTTCAATTTGACACAGTGTGTTGATCAAGTTCCA 1245
1258 ACCAATCCAACCTGTTTCAATTTGACACAGTGTGTTGATCAAGTTCCA 1302

RESULT 3

US-09-248-796A-22
; Sequence 22, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-22

Query Match 58.5%; Score 728.2; DB 4; Length 1536;
Best Local Similarity 74.1%; Pred. No. 6.5e-182;
Matches 922; Conservative 0; Mismatches 323; Indels 0; Gaps 0;

1 AAGACAATCACTGGTGTGTTTGAATAGTTTAAATCAATTAAGTGTGTTTGAATGCTGCTTAAT 60
76 AAGGTTATTACGGGCAATTTTCGATAGTTTAAATTCGTTAATCTTGAACCAATGCTGCTTCT 135
61 TATGCTTTCAAGGCGCCAGGATACCACTTGGAAATGCTGTTTGGGTTGGTCTTATAGAT 120
136 TATTCATATAGAGTCCAGCTAATCTCTACTTGGACCGGTGTAATAGGATGTTCTTTAGAT 195
121 GGTACCACTGCGCAATCCAGGGGATACATTCACATTTGAATATGCCATGTTGTTTAAATAT 180
196 GGAGCTACTGCTAGTGTGCTGTTGACACATTCACGTTAGACATGCCATGTTTTCAAATTT 255
181 ACTATTCACAAACATCTGTTGATTTAACTGCGGATGGTGTGTTAAATATGCTACTTGTCAA 240
256 ATTTACTGATCAAAACGTCATTTAGTTAGTTGCTGATGGTGGTCTTATGCTACTTGTAAAT 315
241 TTTTATTCGGTGTGAGAAATTCACAACTTTTCTACATTAACATGATGTTACTGTGAACGCT 300

RESULT 4

US-09-248-796A-20
; Sequence 20, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:

316 TTGAATCTCTCCGAAGAGTTTACTACTTTTCTAGTGTGTCATGTTCTGACTACTACACA 375
301 TTGAATCATCTCAATTAAGGCAATTTGGTACAGTTTACTTTTACCAATTTGCAATTTCAATTTGGT 360
376 ATGATCTGCTGACACCAAGCCATAGGACATGTAACATTAATCTTCTCAATTCAGTGTGGG 435
361 GGAACAGGTTTCATCAATGATTTTGGAGATTTCTAAATTTTAACTGCTGTTGTTGTTGTTGTTGTT 420
436 GGATCAGGTTTCAGATGTTGATTTGGCAAAATCTCAATGTTTACTCTGCGAGGAATCAATACA 495
421 GTCAATTTAATGATGTTGATTAAGATATCTCAATGATTTGATGTTGTTGTTGTTGTTGTTGTTGTT 480
496 GTTACTTTTAAATGATGTTGATCACTAGCAATTTCCGCAACAGTTGATTTTGAATAAATCAAC 555
481 GTTGATCCAAGTGCATATTTGATGCTTCCAGAGTTATGCAAGTCTCAATTAAGGTCACA 540
556 GTGGCTCCAGGATGATATCTTGTGTTCAAGAAATTTTACCCAGTCTTTCACAGCAGTA 615
541 ACTCTTTTGTGGCACCAATGTTGAAATTTGGTTTACATCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
616 AGTCTTTTCTTCCCAAGAAATGTCAAATGGTTTATATCTCTGTTGTTGTTGTTGTTGTTGTTGTT 675
601 AGTAGTAACCGTGCAGTGTGCTTATGATTTGCTCAATATTCATATTTGTTGTTGTTGTTGTTGTTGTT 660
676 ACTGCTGTTACTGTTGCTACTATAGATTTGTTTCCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 735
661 TTAATGATTTGGAATATTCGGTTTTCATCTGAATCATTTAGTTTACATCACTTAAATCTTTGTTACA 720
736 TTGAATGATTTGGAATATTCGAATTTCTCTGGAATCTTTTCTTCTTACACAGACCTGTTACA 795
721 TCTAATGGAATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
796 TCAACAAGTGTTTTAGTAACTTATCAGAAATGTTCTCTGCGGATATCGTCCATTTGTCGAT 855
781 GCTTATATTTCTGCTACAGATGTTTAAACCAATATATTTAGTATTTAGCATATACCAATGATATAT 840
856 GCTTATGTTTCTGCAACAGGTCAGTCTCATATGCTATGATGATACACTTAATATATATATGCT 915
841 TGTCTGCGAGTCTGCTGCAAGATAAACCTTTTCACTTTTAAGATGGAAGTGGATACAAAGAT 900
916 TGTGTTGGTGGGCTTCTGTTGATGATCTCATTTTACTCATCTTGGCTGGGATATAGTAAT 975
901 AGTATGCGCGGATCTAAGCGGTATTGTGCTAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
976 AGTCAAGCTGTTCTAATGTTTATTTACCAATTTGGTGTAAACCACTAGAACAGTTTACAGACAGT 1035
961 ACCACTGCTGTCACCTTTTACCAATTCATCCAGTGTGATTAACCAAAACCAAAACCAATCGAA 1020
1036 ACCACTGCTGTCACCTTTTACCAATTCATCCAGTGTGATTAACCAAAACCAAAACCAATCGAA 1095
1021 ATTTTGAACCTTATTCGAACCTTACCAATTCATCCAGTGTGATTAACCAAAACCAAAACCAATCGAA 1080
1096 ATTTTGAACCTTATTCGAACCTTACCAATTCATCCAGTGTGATTAACCAAAACCAAAACCAATCGAA 1155
1081 TATCTGACTAGAGTCTGCAACCAATTTGGTGAACAGCTACTGTTATTTGTTGATGTTGCTCATAT 1140
1156 TACCTGACTAGAGTCTGCAACCAATTTGGTGAACAGCTACTGTTATTTGTTGATGTTGCTCATAT 1215
1141 CATCTACCAACCTGTTTACAGTGAATGGACAGGAACCAATCTACTACCAACCAACTCGT 1200
1216 CATCTACTACCACTGTTTACCAAGTGAATGGACAGGAACCAATCTACTACCAACCAACTCGT 1275
1201 ACCAATCCAACCTGTTTCAATTTGACACAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1245
1276 ACCAATCCAACCTGTTTCAATTTGATAGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1320

```

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20
; LENGTH: 3180
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-20

```

Query Match	53.9%	Score 671.6;	DB 4;	Length 3180;
Best Local Similarity	84.5%	Pred. NO. 7.3e-167;		
Matches 755; Conservative	0;	Mismatches 139;	Indels 0;	Gaps 0;

Qy		352	AATGTTGGTGAACAGGTTTCATCAACTGATTGTGGAGAAGATCTCTAAATGTTTTACTGCTGGT	411
Db		37	AATGTAGGTGAACAGGTTCTCTTGTTGATTGTGAAGAATCTCTAAATGTTTTACTGCTGGT	96
Qy		412	ACCAATACAGTCACATTTAATGATGGTGATAAAGATATCTCAAATTTGATGTTGAGTTTCGAA	471
Db		97	ACTAACACAGTTACATTTAATGATGGTGCGAAGAAAATCTCAATTAATGTTGATTTTGGAA	156
Qy		472	AAAGTCAACCCGTTGATCCAAGTGCATATTTGTATGCTTCCAGAGTTTATGCCAAGTCTCAAT	531
Db		157	AGGTCAAAATGTCGATCCAAAGGGTACTTAACTGATTCAGAGTTATATACCAAGTCTCAAC	216
Qy		532	AAAGTCACAACCTCTTTTTGTGGGACCAACAATGTGAAAAATGTTTACACATCTGTGTACAATG	591
Db		217	AAAGTGTCAACTCTCTTTTTGTGTGCACCACAATGTGCAAAATGGTTTACACATCTGTGTACAATG	276
Qy		592	GGGTTCTCCAGTAGTAACGGTGAAGGTTGCTATTTGATTTGCTCAAAATATTTCATATTTGTTATC	651
Db		277	GGATTCGGCTAAACCTTATGGTGGATGTTCAAAATGACTGTTCAAAATATTCATGTTGGTATT	336
Qy		652	ACAAAAGGATTAATAATGATTGGAAATTTATCCGGTTCATCTCGAATCAATTTAGTTTACACTAAA	711
Db		337	ACAAAAGGATTAATAATGATTGGAAATTTATCCGGTTCATCTCGAATCAATTTAGTTTACACCAA	396
Qy		712	ACTTGTACATCTAATGGAAATTCAGATTAAATATCAAAATGTACCTGTGGTTATCGTCCA	771
Db		397	ACTTGTTCATCTAATGGTATCTTTATACATATATAAAAAAGTTCTGTCCGGTTATCGTCCA	456
Qy		772	TTTTATTGATGCTTATATTTCTGCTACAGATGTTAACCAATATATCTTTAGCATATATACCAAT	831
Db		457	TTTGTGTACGCTTATATTTCTGCTACAGATGTTAATTCGTACACCTTGTCTGATGCTAAT	516
Qy		832	GATTATATCTGTGTGGCAGTCGTCGCAAAAGTAAACCTTTTCACTTTAAGATGGACTGGA	891
Db		517	GAATATATCTGTGTGGTGGTTATTTGGCAAAGTGCACCTTTTCACTTAAGATGGACTGGA	576
Qy		892	TACAAGAATAGTGATGTCGGATCTAAACGGTATTTGTCTATGTTGTCTACAACATAGAACAGTT	951
Db		577	TACAGAAATAGTGATGCTGGATCTAAACGGTATTTGTATTTGTGGCTACTTACCAGAACAGTT	636
Qy		952	ACAGACAGTACCACTGCTGTCACTACTTTTACATTTCAATTCGAATCCAAAGTGTGATATAAACCAA	1011
Db		637	ACAGACAGTACTACCGCGCTGACCACTTTACCATTCGATCTTAAACGGGACAAAACTAAG	696
Qy		1012	ACAAATCGAAATTTTTCGAACCTATTTCCAACCACTACCATCACAACTTCATATGTTGGTGTG	1071
Db		697	ACAAATGAAATTTTGAACACCTATTTCACACAACTACAATCAACATCATATGTTGGTGTG	756
Qy		1072	ACTACTTCCTACTGACTAAGACTGCAACAAATGGTGGAAACAGCTACTGTGTTATTTGTTGAT	1131
Db		757	ACTACTTCTTACCTTGACCAAACTGSCAAATTTGGGAAACTGCTACTGTTATTTCTGTTGAT	816

649	AGTCTTGTTGCTCTCAGTGACTGCTGGAGATGCAATCCGGTGTGCTCGGATTTTCA	708
601	AGTAGTAAACGGTGACGTTGCTATTGGATTGCTCAAAATATTCTATATTGGTATCACAAAGGA	660
709	GCAACAAAAGATGATGTGACAAATTGGATTGTTCTACTATACATGTGGGAATAACAAATGGT	768
661	TTAAATGATTGGAAATTATCCGGTTTCATCTGAATCATTTAGTTTACACTAAAACCTGTACA	720
769	TTGAATAGTTTGGAAATATGCCAGTATCATCAGAATCATTTTCTTACCAAAACTTGTGACA	828
721	TCTAAATGGAATTCAGATTTAAATATCAAAATGTACCTGCTGGTTATCGTCCCATTTATTGAT	780
829	CCAACAGITTTTATTACTTATGAAAATGTTTCTCGCAGGTTATCGTCCATTTATTGAT	888
781	GCTT-----ATATTTCTGCTACAGATGTTTAAACCAATATACTTTAGCATATACCAATGAT	834
889	TCTTACGCTGAAAAAATCAGCAACAGCAACGAATGGATTTAAATTTGAATTACACGAATATA	948
835	TATACTTGTGCTGCGAGTCGTCGTCAAAGTAAACCTTTTCACTTTAAGATGGACTGGATAC	894
949	TACAAATTGATGATGCGCAAAAAGGNAATGATCCTCTTATATACTTTTTGGACATCATAC	1008
895	AAGAATAGTGATCCGGATCTAAACGGTATTTGTCATTGTTGCTCAAACTAGAAACAGTTTACA	954
1009	ACAAATAGTGATGCGAGATCCAAATGGAGCTGCGGTAGTTGTTTACTACGAAACAGTCACT	1068
955	GACAGTACCACCTGCTGCTCACTCTTTTACCATTCAATCCCAAGTGTGCTATAAAACCAAAACA	1014
1069	GATTCTACAACAGCAATTTACCAATTACCGTTTGATCCCAAGTTGATAAACAACAAACC	1128
1015	ATCGAAATTTTGCAACCTTATCCAAACCACTACCATTCAACTTTCATATGTTGGTGTGACT	1074
1129	ATTGAGATAATAGAACCCATCCCTACTACCACATTACTACTTTCATATGTTGGGATTTCT	1188
1075	ACTTCTTATCTGATAAGATCGACCAATTTGGTGGAACAGCTACTGTTATTGTTGATGTC	1134
1189	ACTTCACTTTCTACGAAGATGCAACTTAATTGGAGGGAACAGCAACTGTTGTTGTTGATGT	1248
1135	CCATATCATACTACTACCAACTGTTTACCAGTGAATTGGACAGGAACAAATCACTACCAACACA	1194
1249	CCCTATCATTAACAATCACTACATATCATATGATATATGACTGATCACTACCATCAATCAAGT	1308
1195	ACTCGTACCAATCCAACTGATTTCAATTGACACAGTGGTGTACAGTTCCA	1245
1309	ACTTATACAAATCCCACTGACTCGATTGGATTGATACAGTTGTTGTTGACAAGTTCCA	1359

RESULT 6

```

US-09-248-796A-2142
; Sequence 2142, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2142
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (866)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-248-796A-2142

```

Query Match	40.9%;	Score 509.8;	DB 4;	Length 900;
Best Local Similarity	82.3%;	Pred. No. 1.9e-124;		
Matches 610;	Conservative 0;	Mismatches 127;	Indels 4;	Gaps 2;
Qy	506	CTTCCAGAGTTATGCCAAAGTCTCAATAAGGTCACAACTCTTTTGTGGC-ACCACAATGT	564	
Db	1	CGTCAAGACTTATTCCAAAGTATTAACAAAGCTTCAATCACTTATGTGGCAACCAAAATGT	60	
Qy	565	GAATAATGGTTACACATCTCGGTACAAATGGGGTTCTCAGTAGTAAACGGTGAAGTGGCTATT	624	
Db	61	GCAAAATGGCTACACATCTGGTGCNAATGGGGTTCATAGTTCTCTCAGTGGTGACACTACTATT	120	
Qy	625	GATTGTCTCAAAATTCATATTTGGTATCACAAAAGGATTAATAATGATTGGAAATTTACCGGTT	684	
Db	121	GACTGTTCAAAATGTTCAATTTGGTATPAAANAGGATTAATAATGATTGGAAATTTTCGGGTA	180	
Qy	685	TCATCTGAATCAATTTAGTTTACACTAAAACTTTGTAATCTAAATGGAATTCAGATTAATAAT	744	
Db	181	TCCTCTGATTCATTAAGTTTACAATAAAACTTGTTCATCTACAGGTATTTCTATCACATAT	240	
Qy	745	CAAAATGTACCTGCTCGTTATCGTCCATTTATTTGATGCTTATATTTCTGCTACAGATGTT	804	
Db	241	GAAAATGTTCCCGCTGGTTATCGTCCATTTTTTGGAGCTATATACTCTGGTGTGAGACCAG	300	
Qy	805	AACCAATATACTTTAGCATATACCAATGATTATACTTTGTCTGGCAGTCTCTGCAAAAGT	864	
Db	301	AACAGACA---ATTAAANATACTAATGATTATGCTGTGTGGTAGTTCCTTACAAAGT	357	
Qy	865	AAACCTTTCACTTTTAAGATGGAATCGGATACAAAGATAGTGAATGCCGGATCTAAGCGTATT	924	
Db	358	AAGCCGTTCAATTTAAGATTGGAGAGGATACAAATAATAGTGAAGCTAAATCTTAAACGGTTTT	417	
Qy	925	GTCAATTTGCTTACAACATAGACAGTTACAGACAGTACCACCTGCTGTCACCTACTTTTACCA	984	
Db	418	GTCAATTTGTTGCTACAAACCCGGACAGTTACTGACAGTACTACTGCTGTCTACTTTTACCT	477	
Qy	985	TTCAATCCAAAGTGTGTGATTAATAACCAAAACAATCGAAATTTTGGCAACCTATTCCAACCACT	1044	
Db	478	TTTAAATCCAAAGTATTGCAAAACCAAAACAATCGAAATTTTGGCAACCTATTCCAACAACC	537	
Qy	1045	ACCATCAAACTTTCAATATGTTGGTGTGAATTAATTCCTTCTGACTAAGACTGACCAATTT	1104	
Db	538	ACTATCACAACTTTCATATGTTGGTGTGAGTACTTCGTACCTGTGACTTAAATCTGACCAATTT	597	
Qy	1105	GGTGAACAGCTACTGTTATTTGTTGATGTGCCATATCATATACTACCAACTGTTTACCAGT	1164	
Db	598	GGTGAACAGCTACTGTTATTTGTTGATGTGCCATATCATATACTACCAACTGTTTACCAGT	657	
Qy	1165	GAATGGACAGGAACAATCACTACCAACCAAACTCGTACCAATCCAATCGAATTCGAATTCAC	1224	
Db	658	GAATGGACAGGAACAATCACTACCACTACCAACTCGTACCAATCCAATCCAATCTGATTCTATAGAT	717	
Qy	1225	ACAGTGGTGTGAACAAGTTCCA	1245	
Db	718	ACTGTGCTGTGCAAGTTCCA	738	

RESULT. T 7

RES001 /
 US-09-248-796A-2595
 ; Sequence 2595, Application US/09248796A
 ; Patent NO. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstein et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248.796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208

```

; SEQ ID NO 2595
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2595

Query Match      33.3%; Score 414.6; DB 4; Length 690;
Best Local Similarity 81.1%; Pred. No. 2e-99;
Matches 494; Conservative 0; Mismatches 114; Indels 1; Gaps 1;

QY 7 ATCACTGGTGTGTTTTCATAGTTTAAATTCATTAACCTGCTGCTCCAAATGCTTAATTATGCT 66
DB 82 ATTACGGGTGTTTTCATAGTTTTCATAGTTTTCATAGTTTTCATAGTTTTCATAGTTTTCAT 141
QY 67 TTCAAAGGGCCAGGATACCCAACTTGGAAATGCTGTTTGGGTGCTGCTTATAGATGGTACC 126
DB 142 TATAAGGGCCAAATAGACCAACTTGGAAATGCTGTTTGGGTGCTGCTTATAGATGGTACT 201
QY 127 AGTGCCAAATCCAGGGGATACATTCACATTTGAATATGCCATGCTGTTTAAATATATCTACT 186
DB 202 AGTGCCAAATCCAGGAGACATTCACATTTGAATATGCCATGCTGTTTAAATATATCTACT 261
QY 187 TCACAAACATCTGTTGATTTTAACTTCCGATGCTGTTTAAATATGCTTCTGCTCAATTTTAT 246
DB 262 GATCAAAACATCTGTTGATTTGACTGCTGAAGGTGTTTAAATATGCTTACATGCTGCTTTAT 321
QY 247 TCTGGTGAAGAATTCACAACTTTTCTACATTAACATGCTACTGTGAACGACGCTTTGAAA 306
DB 322 TCAGGTGAAGAATTTACAACATTTTCTTCATTTAAATGTAATGCTGAGCAATCTTTAAACA 381
QY 307 TCATCCATTAAGCAATTTGGTACAGTTACTTTTACCAATGCAATTCATGTTGGTGGGAACA 366
DB 382 TCATCTATTAAAGGCTTTGGTACGGTACTTTTACCCTTTTCAATTAATGTTGGTGGGAACA 441
QY 367 GGTTCATCAACTGATTTGGAAGATCTTAAATGTTTACTGCTGCTGCTGCTGCTGCTGCTGCT 426
DB 442 GGTTCATCGGTTGATTTGGAATTTCTCAATGTTTAAAGGCTGGCCACCAACACAGTTTACT 501
QY 427 TTTAAATGATGGTGAATAAGATATCTCAATTTGATGTTTGAAGTCTCAACGCTTTGAT 486
DB 502 TTTAAATGATGGTGAATAAGATATCTCAATTTGATGTTTGAAGTCTCAACGCTTTGAT 561
QY 487 CCAAGTGCAATTTGATGCTTCCAGAGTTATGCCAAGTCTCAATTAAGGTCACAACTCTT 546
DB 562 GCAAGTGCAATTTTTCATAGCTCAAGCTTATTTCCAGTATTTAAACAAAGCTTCAATCACT 621
QY 547 TTTGTGCTG-ACCAATGTAAGAAATGGTTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
DB 622 TATGTGCAACCAACCAATGTCAAATGGCTTACATCTGCTGCAATGGGTTTCATAGTTCT 681
QY 606 TNAAGGTGA 614
DB 682 CACTGGTGA 690

RESULT 8
US-09-248-796A-2141
; Sequence 2141, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074, 725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096, 409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2141
; LENGTH: 2436

```



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/ GENERAL INFORMATION:
/ APPLICANT: Keith Weinstock et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
/ TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 9483
/ LENGTH: 294
/ TYPE: DNA
/ ORGANISM: Candida albicans
/ US-09-248-796A-9483

Query Match      12.0%; Score 149.8; DB 4; Length 294;
Best Local Similarity 73.9%; Pred. No. 8.5e-30;
Matches 190; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 226 TATGCTACTTGTCAATTTATTCGTGGAAGAATTCACAACTTTTTCATCAATTAACATGT 285
Db 293 TATGCCACTTGTGACTTTAATGCTGTGGAAGAATTTACGACATTTTCTCCATTATCATGT 234

Qy 286 ACTGTGAACGACGCTTTGAATCATCCATTAAGGCATTTGTCAGTACTTTTACCAATT 345
Db 233 AGTGTGAACAGTGTTCCTGGTATCATATGCTAGGGTTTCTGGTAGGTCAAATGGCCCAT 174

Qy 346 GCATTCAATGTGTGGGAACAGGTTTCATCACTGATTTGGAAGATTTCTAAATGTTTACT 405
Db 173 ACATTCAATGTAGTGGGAACAGGTTCTTCAGTTGATTTGGCAGATTTCCAAATGTTTACT 114

Qy 406 GCTGGTACCATAACAGTCACATTTAATGATGGTGGAATAAAGATATCTCAATGATGTTGAG 465
Db 113 GCCGGAATAAACAACACTGTGACTTTTCATGGATGGCGATACAAAGATTTCTACCACCTGTTGAT 54

Qy 466 TTTGAAAAGTCAACCGT 482
Db 53 TTTGACGGTCTCCAGT 37

RESULT 12
US-08-145-705A-32/c
; Sequence 32, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: German P 42 36 708.5
; APPLICATION NUMBER: 33,141
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
```

```
/ FILING DATE: October 30, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kurt G. Briscoe
/ REGISTRATION NUMBER: 33,141
/ REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (914) 332-1700
/ TELEFAX: (914) 332-1844
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 100 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Candida albicans
/ US-08-145-705A-32

Query Match      6.6%; Score 82.4; DB 1; Length 100;
Best Local Similarity 89.0%; Pred. No. 3.1e-12;
Matches 89; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1119 TGTATTGTTGATGTGCCATATCATCTACTACCACTGTGTACCACTGTAATGGACAGGAAC 1178
Db 100 TGTATTGTTGATGTGCCATATCATCTACTACCACTGTGTACCACTGTAATGGACAGGAAC 41

Qy 1179 AATCACTACCAACCAACTCGTACCAATCCAACTCAATTCATTC 1218
Db 40 AATCACTACTACTACCAACAACTAATCCAACTGTTCA 1

RESULT 13
US-08-145-705A-34/c
; Sequence 34, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: German P 42 36 708.5
; APPLICATION NUMBER: 33,141
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
```


TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-145-705A-34

Query Match 6.6%; Score 82.4; DB 1; Length 100;
Best Local Similarity 89.0%; Pred. No. 3.1e-12;
Matches 89; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 919 GGTATTGTTCATTTGCTTACAACTAGAACAGTTACAGACAGTACCACTGCTGTGCTACT 978
DB 100 GGTATTGTTCATTTGCTTACAACTAGAACAGTTACAGACAGTACCACTGCTGTGCTACT 41
QY 979 TTACCAATTCATCCAGTGTGATTAACCAACCAAAACAATCG 1018
DB 40 TTACCAATTCATCCAGTGTGATTAACCAACCAAAACAATG 1

RESULT 14
US-08-145-705A-33/c
; Sequence 33, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-145-705A-33
Query Match 6.1%; Score 76; DB 1; Length 100;
Best Local Similarity 85.0%; Pred. No. 1.5e-10;
Matches 85; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1019 AAATTTTGAACCTATTTCGAACCACTACCACTACCACTCATATGTTGGTGTGACTACTT 1078
DB 100 AAATTTTGAACCACTATTTCGAACCACTACCACTACCACTCATATGTTGGTGTGACTACTT 41
QY 1079 CCTATCTGACTAGACTGCACCAATTTGGTGAACACAGCTAC 1118
DB 40 CCTACAGACCAACTGTACCAATAGGACAACTGCTAC 1

RESULT 15
US-08-145-705A-36/c
; Sequence 36, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-145-705A-36
Query Match 5.5%; Score 68; DB 1; Length 100;
Best Local Similarity 80.0%; Pred. No. 1.9e-08;

	Matches	80;	Conservative	0;	Mismatches	20;	Indels	0;	Gaps	0;
Qy	719	CATCTAATGGAATTCAGATTAAATATCAAAATGTACCTGCTGGTTATCGTCCATTATTG	778							
Db	100	CATCTAATGGTAICTCTATCACATATGAAATATCCCTGCAGGTTATCGTCCATTATTG	41							
Qy	779	ATGCTTATATTTCTGTACAGATGTTAACCAATATACTTT	818							
Db	40	ACGTTTATGTATCTGCTCCGGAIGTTAAACAGTATATTTT	1							

Search completed: March 24, 2005, 06:07:24
Job time : 182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 17:51.23 ; Search time 182 Seconds
(without alignments)
2677.572 Million cell updates/sec

Title: US-09-715-876-8

Perfect score: 6495

Sequence: 1 MLQQFTLLFLYLSASAKTI.....SIHQSTWLYGLTLLSLFI 1360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 40 summaries

Database : A Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6465	99.5	1260	7 ABW01168	Candida a
2	4204.5	64.7	1119	7 ABW01170	Candida a
3	3938.5	60.6	1047	7 ABW01175	Candida a
4	2680.5	41.3	1443	7 ABW01173	Candida a
5	2584.5	39.8	1270	7 ABW01172	Candida a
6	2452.5	37.8	2297	7 ABW01174	Candida a
7	1992.5	30.7	468	7 ABW01169	Candida a
8	1819	28.0	469	7 ABW01171	Candida a
9	1717.5	26.4	468	7 ABW01176	Candida a
10	939	14.5	1537	8 ADP87475	S cerevis
11	939	14.5	1537	8 ADN18745	Bacterial
12	938	14.4	1537	2 AAR60562	Yeast 4.7
13	932.5	14.4	1322	8 ADN18700	Bacterial
14	721.5	11.1	5179	4 AAM24516	C899p pre
15	721.5	11.1	5179	6 ABP55365	Human col
16	721.5	11.1	5179	6 ABO07258	Human p53
17	721.5	11.1	5179	7 ADD48091	Human Pro
18	721.5	11.1	5179	7 ADD44998	Human Pro
19	721.5	11.1	5179	8 ADG29695	Human col
20	721.5	11.1	5179	8 ADG80379	Intestina
21	711	10.9	1075	8 ADS43638	Bacterial
22	685	10.5	2586	4 ABB66878	Drosophil
23	668.5	10.3	778	4 ABU53143	Human tes
24	665	10.2	770	4 ABU53141	Human tes
25	658	10.1	1831	6 ABU43109	Protein e

26	658	10.1	1870	6	ABJ19019	Pathogen
27	657.5	10.1	717	4	ABU53150	Human tes
28	657.5	10.1	717	4	ABU53149	Human tes
29	657.5	10.1	717	4	ABU53151	Human tes
30	657.5	10.1	717	4	ABU53145	Human tes
31	657.5	10.1	717	4	ABU53148	Human tes
32	657.5	10.1	717	4	ABU53147	Human tes
33	657.5	10.1	717	4	ABU53146	Human tes
34	655.5	10.1	745	4	ABU53142	Human tes
35	651	10.0	2137	5	ABP39618	Staphyloc
36	651	10.0	2137	8	ADS05656	Staphyloc
37	646.5	10.0	2271	6	ABM72734	Staphyloc
38	646.5	10.0	2283	6	ABP56876	Staphyloc
39	640.5	9.9	2261	6	ABJ18914	Pathogen
40	640.5	9.9	2344	4	AAU37120	Staphyloc
41	637.5	9.8	2271	6	ABU16000	Protein e
42	632.5	9.7	4315	5	ABP43908	MUC5B par
43	624	9.6	800	8	ABO58564	Human gen
44	618.5	9.5	5703	8	ADL23265	Human MUC
45	615.5	9.5	695	4	ABU53152	Human tes

ALIGNMENTS

RESULT 1

ABW01168
ID ABW01168 standard; protein; 1260 AA.

XX AC ABW01168;

XX DT 15-JAN-2004 (first entry)

XX DE Candida albicans agglutinin-like sequence (ALS) 1 protein.

XX KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;

XX OS candidiasis; vaccine; fungicide.

XX OS Candida albicans.

XX FN US2003124134-A1.

XX PD 03-JUL-2003.

XX PF 13-SEP-2002; 2002US-00245802.

XX PR 19-NOV-1999; 99US-0166663P.

XX PR 18-NOV-2000; 2000US-00715876.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.

XX N-PSDB; RAD62305.

XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
the organism.

XX Disclosure; Page 14-17; 65pp; English.

XX The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) protein

XX Sequence 1260 AA;

Query Match		99.58;	Score 6465;	DB 7;	Length 1260;	
Best Local Similarity		99.68;	Pred. No. 0;			
Matches 1255;		Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;	
Qy	1	MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWNSAANYAFKPGYPTWNAVLGWSLDGTS	60			
Db	1	MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWNSAANYAFKPGYPTWNAVLGWSLDGTS	60			
Qy	61	ANPGDTFTLAMPVCVKYKTTSGTSVDLTADGVKATCOFYSGEBFTTFSTLTCTVNDALKS	120			
Db	61	ANPGDTFTLAMPVCVKYKTTSGTSVDLTADGVKATCOFYSGEBFTTFSTLTCTVNDALKS	120			
Qy	121	SIKAFGVTTLPIAFNVCGTSSDLEDSKCFCTAGTNTVTFDGDGKDISIDVBEKSTVDP	180			
Db	121	SIKAFGVTTLPIAFNVCGTSSDLEDSKCFCTAGTNTVTFDGDGKDISIDVBEKSTVDP	180			
Qy	181	SAYLIASRVMPSLMKVTTLFAPOCENGYSCTGTMGFSSNGDVAIDCSNIHIGITKGLND	240			
Db	181	SAYLIASRVMPSLMKVTTLFAPOCENGYSCTGTMGFSSNGDVAIDCSNIHIGITKGLND	240			
Qy	241	WNPVSSSESFTYKTCISNGIQIKYQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG	300			
Db	241	WNPVSSSESFTYKTCISNGIQIKYQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG	300			
Qy	301	SRLOSKEPTLRWTCYKNSDAGSGIVIVATRTVDSSTTAVTTLPEPNSVDKTKTIEILQ	360			
Db	301	SRLOSKEPTLRWTCYKNSDAGSGIVIVATRTVDSSTTAVTTLPEPNSVDKTKTIEILQ	360			
Qy	361	PIPTTTITTSVGVTTSYLAKTAPIGETATVIVDVPYHHTTTVTSEWGTGTTTTTTRNP	420			
Db	361	PIPTTTITTSVGVTTSYLAKTAPIGETATVIVDVPYHHTTTVTSEWGTGTTTTTTRNP	420			
Qy	421	TDSIDTIVVQVPLDNPFTVSTTEYWSQSFATTTVTAPPGGTDVVIIREPPNHTVTTTEYW	480			
Db	421	TDSIDTIVVQVPSNPVTSTTEYWSQSFATTTVTAPPGGTDVVIIREPPNHTVTTTEYW	480			
Qy	481	SQSFAATTTVTAPPGGTDVLIIREPPNPTVTTTEYWSQSFATTTVTAPPGGTDVLIIRE	540			
Db	481	SQSFAATTTVTAPPGGTDVLIIREPPNPTVTTTEYWSQSFATTTVTAPPGGTDVLIIRE	540			
Qy	541	PPNPTVTTTEYWSQSFATTTVTAPPGGTDVLIIREPPNPTVTTTEYWSQSFATTTVT	600			
Db	541	PPNPTVTTTEYWSQSFATTTVTAPPGGTDVLIIREPPNPTVTTTEYWSQSFATTTVT	600			
Qy	601	PPGTDVLIIREPPNHTVTTTEYWSQSFATTTVTGPPSGTDVVIIREPPNPTVTTTEYW	660			
Db	601	PPGTDVLIIREPPNHTVTTTEYWSQSFATTTVTGPPSGTDVVIIREPPNPTVTTTEYW	660			
Qy	661	SQSFAATTTVTAPPGGTDVLIIREPPNHTVTTTEYWSQSFATTTVTAPPGGTDVLIIRE	720			
Db	661	SQSFAATTTVTAPPGGTDVLIIREPPNHTVTTTEYWSQSFATTTVTAPPGGTDVLIIRE	720			
Qy	721	PPNHTVTTTEYWSQSFATTTVTAPPGGTDVLIIREPPNPTVTTTEYWSQSFATTTVT	780			
Db	721	PPNHTVTTTEYWSQSFATTTVTAPPGGTDVLIIREPPNPTVTTTEYWSQSFATTTVT	780			
Qy	781	PPGTDVLIIREPPNHTVTTTEYWSQSFATTTVTGPPSGTDVVIIREPPNPTVTTTEYW	840			
Db	781	PPGTDVLIIREPPNHTVTTTEYWSQSFATTTVTGPPSGTDVVIIREPPNPTVTTTEYW	840			
Qy	841	SSDGMLSSSTLVTSEFTTTELCSDGKCSRSSSGIVTNPDNSSSTVTSVTPAST	900			
Db	841	SSDGMLSSSTLVTSEFTTTELCSDGKCSRSSSGIVTNPDNSSSTVTSVTPAST	900			
Qy	901	MSDSLSTDGIATSNDVSKSGSVTTTSTVTTIQTTPNPLSSVTSLTQLSSIPVSE	960			
Db	901	MSDSLSTDGIATSNDVSKSGSVTTTSTVTTIQTTPNPLSSVTSLTQLSSIPVSE	960			
Qy	961	SESKVTTTSGNDQSGTHDSQSTTEIEIVTTSSTKVLPPVSSNTDLTSEPTNTREOPT	1020			
Db	961	SESKVTTTSGNDQSGTHDSQSTTEIEIVTTSSTKVLPPVSSNTDLTSEPTNTREOPT	1020			
Query Match		64.78;	Score 4204.5;	DB 7;	Length 1119;	
Best Local Similarity		64.98;	Pred. No. 4.8e-209;			
Matches 844;		Conservative 106;	Mismatches 128;	Indels 223;	Gaps 18;	
Qy	1	MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWNSAANYAFKPGYPTWNAVLGWSLDGTS	60			
Db	1	MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWNSAANYAFKPGYPTWNAVLGWSLDGTS	60			
RESULT 2						
ABW01170						
ID	ABW01170	standard; protein; 1119 AA.				
XX						
AC	ABW01170;					
XX						
DT	15-JAN-2004	(first entry)				
XX						
DE		Candida albicans agglutinin-like sequence (ALS) 3 protein.				
XX						
KW		Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;				
KW		candidiasis; vaccine; fungicide.				
XX						
OS		Candida albicans.				
XX						
PN	US2003124134-A1.					
XX						
PD	03-JUL-2003.					
XX						
PF	13-SEP-2002; 2002US-00245802.					
XX						
PR	19-NOV-1999; 99US-0166663P.					
PR	18-NOV-2000; 2000US-00715876.					
XX						
PA	(HARB-) HARBOR-UCLA RES & EDUCATION INST.					
XX						
PI	Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;					
XX						
DR	WPI; 2003-810971/76.					
DR	N-PSDB; AAD62307.					
XX						
PT	New monoclonal antibody against Candida albicans agglutinin-like sequence					
PT	1 adhesin proteins, for use as a vaccine to treat or prevent disseminated					
PT	candidiasis, or to generate an immune response that blocks adherence of					
PT	the organism.					
XX						
PS	Disclosure; Page 21-23; 65pp; English.					
XX						
CC	The present invention relates to a monoclonal antibody against an					
CC	agglutinin-like sequence (ALS)1 protein that specifically binds an					
CC	epitope in an N-terminal domain and which inhibits adherence of Candida					
CC	albicans to endothelial cells. The invention is useful as vaccines for					
CC	treating and preventing disseminated candidiasis and for generating an					
CC	immune response capable of blocking adherence of the organism. The					
CC	invention is also useful in gene therapy. The present sequence is Candida					
CC	albicans agglutinin-like sequence (ALS) protein					
XX						
SQ	Sequence 1119 AA;					

Qy 61 ANPGDTFTLNNPCVFKYKTSQTSVDLTADGVKXATCOFYSGERTFTSTLTCTVNDALKS 120
Db 61 ASPGDTFTLNNPCVFKYKTSQTSVDLTADGVKXATCOFYSGERTFTSTLTCTVNDALKS 120
Qy 121 SIKAFGTVTLPIAFNVGSGTSDLEDSKCFAGTNTVTFNDGDKDISIDVEPKSTVDP 180
Db 121 SIKALGTVTLPIAFNVGSGTSDLEDSKCFAGTNTVTFNDGDKDISIDVEPKSTVDP 180
Qy 181 SAYLIASRUMPSINKVTLFVAPOCENGYSGTGPFSSNGDVAIDCSNIHIGTKGLND 240
Db 181 KGYLTDSRVIPSLNKNVTLFVAPOCANGYSGTGPFSSNGDVAIDCSNIHIGTKGLND 240
Qy 241 WNPVSSPSYTKTCSNGIQIKYONVAGRPFDIAYISATDVNOVTLAYTNDYTCAG 300
Db 241 WNPVSSPSYTKTCSNGIPFYKXNPAGRPFDVAYISATDVNSYTLSEYNEVCAG 300
Qy 301 SRLQSKPFTLRWTKYNSDAGSNGIIVATRTVTDSTTAVTTLPPNPSVDKTKIILQ 360
Db 301 GYMQRAPFTLRWTKYNSDAGSNGIIVATRTVTDSTTAVTTLPPNPSVDKTKIILQ 360
Qy 361 PIPTTTITTSVGTTSVLTAKIETATVIVDPVPHHTTTTSEWGTGTTTTTTHNP 420
Db 361 PIPTTTITTSVGTTSVLTAKIETATVIVDPVPHHTTTTSEWGTGTTTTTTHNP 420
Qy 421 TDSIDTVVQVPLNPPTVSTTEYWSQSPATTTTITAPPGGTDTVIIRPPNHTVTTTEY 480
Db 421 TDSIDTVVQVPSNPPTVSTTEYWSQSPATTTTITAPPGGTDTVIIRPPNHTVTTTEY 480
Qy 481 SQSPATTTTITAPPGGTDSVIRPPNPTVTTTEYWSQSPATTTTITAPPGGTDSVIR 540
Db 481 SESYTTSTFTAPGGTDSVIRPPNPTVTTTEYWSQSPATTTTITAPPGGTDSVIR 540
Qy 541 PPNTVTTTEYWSQSYATTTTITAPPGGTDSVIRPPNHTVTTTEYWSQSYATTTTIT 600
Db 541 PPNTVTTTEYWSQSYATTTTITAPPGGTDSVIRPPNHTVTTTEYWSQSYATTTTIT 600
Qy 601 PRGGTDTVIIRPPNHTVTTTEYWSQSPATTTTITAPPGGTDTVIIRPPNHTVTTTEY 660
Db 601 PRGGTDTVIIRPPNHTVTTTEYWSQSPATTTTITAPPGGTDTVIIRPPNHTVTTTEY 660
Qy 661 SQSVATTTTITAPPGETDTVL-----IRE 684
Db 661 SQSVATTTTITAPPGETDTVLIRPPNHTVTTTEYWSQSPATTTTITAPPGETDTVL 720
Qy 685 PPNTVTTTEYWSQSYATTTTITAPPGGTDTVLIRPPNHTVTTTEYWSQSYATTTTIT 744
Db 721 PPNTVTTTEYWSQSYATTTTITAPPGGTDTVLIRPPNHTVTTTEYWSQSYATTTTIT 780
Qy 745 PRGGTDTVIIRPPNHTVTTTEYWSQSPATTTTITAPPGGTDTVIIRPPNHTVTTTEY 804
Db 781 PRGGTDTVIIRPPNHTVTTTEYWSQSPATTTTITAPPGGTDTVIIRPPNHTVTTTEY 836
Qy 805 DITSIPFSRPHYVNSTSDISTPSSSMNTPTSISDGMLLSTTLVTSSETTELIC 864
Db 837 -----SFSRPHYVNT-----LMSVTIETKITETSC 866
Qy 865 SDGKCSRLLSSSGSVTPNDNESSIVTVPFTASTMSDSLSSTGIGATSSDNVSKGV 924
Db 867 EGDGKCSMVSVSTRIVTPNNIETPMVNTVDSVTTESTS-QSPSGI-----FSESGV 918
Qy 925 SVTHTTS-VTIIOTPNPLSSVSLTQISIPSVSESKVTFTSNGDNGSGTHDSOST 983
Db 919 SVTESSTVTTTAQTN-----PSVPTTESKEVFTTKGNENGPEPSPT 961
Qy 984 STEIIVTSSKVLPPVNVSSNDLTSEPTNREQTTLSTNSITDIITTSQPTGNG 1043
Db 962 N-----VKSMDSNSEPT----- 974
Qy 1044 DNTSSTNPVPTVATSTLASASEDNKSGHESASTSLKPSMGNSGLTSTTEIE---ATT 1100
Db 975 -----TSTAAS-----TSDIENETIAT 992

Qy 1101 TSPTAPSPAVSGSDVTTEPTDTRREQPTTLSTTKNSLVAQTATNEN-GKSPSTD 1159
Db 993 TGSVEASSPISSADET-----TTVTTTAEBSVI---EQPTNNGGKAPSA- 1038
Qy 1160 LTSSTLTGTSASANSSELVTSVTCGAVASANDOSHSTSVTNSNSIVSNTPTQTLTQ 1219
Db 1039 -----TSSPSTTTTANNDSVITG-----TTSTNQSOSQSYN-----SDTQOQTLSQ 1080
Qy 1220 QVTSSSPSTWTFIATYDGSIIQHSHTWLYGLITLISLFI 1260
Db 1081 QMTSSLSVSLH--MLTTFDGSVSIQHSHTWLYGLITLISLFI 1119
RESULT 3
ABW01175
ID AEW01175 standard; protein; 1047 AA.
AC ABW01175;
XX
XX 15-JAN-2004 (first entry)
XX
XX Candida albicans agglutinin-like sequence (ALS) 8 protein.
XX
XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
XX
XX candidiasis; vaccine; fungicide.
XX
XX Candida albicans.
XX
XX US2003124134-A1.
XX
XX 03-JUL-2003.
XX
XX 13-SEP-2002; 2002US-00245802.
XX
XX 19-NOV-1999; 99US-0166663P.
XX
XX 18-NOV-2000; 2000US-00715876.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX
XX WPI; 2003-810971/76.
XX
XX N-PSDB; AAD62312.
XX
XX New monoclonal antibody against Candida albicans agglutinin-like sequence
XX
XX 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
XX
XX candidiasis, or to generate an immune response that blocks adherence of
XX
XX the organism.
XX
XX Disclosure; Page 48-50; 65pp; English.
XX
XX The present invention relates to a monoclonal antibody against an
XX
XX agglutinin-like sequence (ALS)1 protein that specifically binds an
XX
XX epitope in an N-terminal domain and which inhibits adherence of Candida
XX
XX albicans to endothelial cells. The invention is useful as vaccines for
XX
XX treating and preventing disseminated candidiasis and for generating an
XX
XX immune response capable of blocking adherence of the organism. The
XX
XX invention is also useful in gene therapy. The present sequence is Candida
XX
XX albicans agglutinin-like sequence (ALS) protein
XX
XX Sequence 1047 AA;
Query Match 60.6%; Score 3938.5; DB 7; Length 1047;
Best Local Similarity 63.7%; Pred. No. 2.6e-195;
Matches 806; Conservative 116; Mismatches 120; Indels 223; Gaps 18;
Qy 1 MLQOFTLLFLVLSIASAKTITGVFDSFNSLTWSNAANYAFKPGYPTWNAVGLMSLDGTS 60
Db 1 MLQOFTLLFLVLSIASAKTITGVFDSFNSLTWSNAANYAFKPGYPTWNAVGLMSLDGTS 60
Qy 61 ANPGDTFTLNNPCVFKYKTSQTSVDLTADGVKXATCOFYSGERTFTSTLTCTVNDALKS 120
Db 61 ASPGDTFTLNNPCVFKYKTSQTSVDLTADGVKXATCOFYSGERTFTSTLTCTVNDALKS 120

```
121 SIKAFGVTLPIAFNVGGTSSDLEDSKCFAGTNTVTFNDGKDOIISDVPEKSTVDP 180
121 SIKALGVTLPIAFNVGGTSSDLEDSKCFAGTNTVTFNDGKKIISINVDFERSNDP 180
181 SAYLYASRVNPSLKNVTLFVAPQCENGYTSGTMFSSNGDVAIDCSNIHIGITKGLND 240
181 KGVLTDSRVIPSLKNVSTLFPVAPQCANGYTSGTMGFANTYGDVQIDCSNIHVGITKGLND 240
241 WNPVSSSESYKTKCTSNIGIQIKQNVAGYRPFIDAYISATDVNQYTLAYTNDVTCAG 300
241 YNPVSSSESYKTKCTSNIGIFITYKNVAGYRPFVDAYISATDVNSYTLAYANEYTCAG 300
301 SRLQSKPTLRWTCYKNSDAGSNGIVAVTRVTDSTTAVTTLFPNPSVDKTKTIELQ 360
301 GYQRAPTLRWTCYKNSDAGSNGIVAVTRVTDSTTAVTTLFPDNRDKTKTIELK 360
361 PIPTTTITTSYGVGVTTSYLTAKTAPIGETATVIDVPYHTTTTTSVETGTTTTRTNP 420
361 PIPTTTITTSYGVGVTTSYLTAKTAPIGETATVIDVPYHTTTTTSVETGTTTTRTNP 420
421 TDSIDTVVQVPLBNPTVSTTEYWSQSFATTTVTPPGCTDVTIIRPPNHTVTTTEYW 480
421 TDSIDTVIVQVPSNPVTTTTEYWSQSFATTTITGPPGNTDVLIRPPNHTVTTTEY 480
481 SQSFATTTTVPAPGGTDSVLIIRPPNPTVTTTTEYWSQSFATTTVTPPGTDSVLI 540
481 SESYTTTSTTAPPGTDSVLIIRPPNPTVTTTTEYWSQSFATTTSTFTAPPGTDSVLI 540
541 PPNETVTTTTEYWSQSFATTTTVPAPGGTDSVLIIRPPNHTVTTTTEYWSQSFATTTV 600
541 PPNETVTTTTEYWSQSFATTTTVPAPGGTDSVLIIRPPNHTVTTTTEYWSQSFATTTV 600
601 PPGCTDVTIIRPPNHTVTTTTEYWSQSFATTTVTPPGTDSVLIIRPPNHTVTTTEYW 660
601 PPGCTDVTIIRPPNHTVTTTTEYWSQSFATTTVTPPGTDSVLIIRPPNHTVTTTEYW 624
661 SQSFATTTTVPAPGGTDSVLIIRPPNHTVTTTTEYWSQSFATTTVTPPGTDSVLI 720
625 SQSFATTTTVPAPGGTDSVLIIRPPNHTVTTTTEYWSQSFATTTVTPPGTDSVLI 684
721 PPNETVTTTTEYWSQSFATTTTVPAPGGTDSVLIIRPPNHTVTTTTEYWSQSFATTTV 780
685 PPNETVTTTTEYWSQSFATTTTVPAPGGTDSVLIIRPPNHTVTTTTEYWSQSFATTTV 744
781 PPGCTDVTIIRPPNHTVTTTTEYWSQSFATTTVTPPGTDSVLIIRPPNHTVTTTEYW 840
745 PPGCTDVTIIRPPNHTVTTTTEYWSQSFATTTVTPPGTDSVLIIRPPNHTVTTTEYW 776
841 SSDGMLLSTLVTSETTTTLICS DGKCSRLSSSGIVTNPDNSBESSIVTSTVPTAST 900
777 -----LYSTTVYVETKTIETSTCEGKGSVSVSTRIVIPNNIETPMVNTVDSVTT 830
901 MSDLSSTDGSISATSDNVKSGSVVTTTS-VTTIQTTPNPLSSSVTSITQLSIPSVS 959
831 ESTS-QSPSGI-----FSSGVSVESTSTVTTAQTN-----PSVP 865
960 ESEKVTFTSNGDNQSGTHDSQSTSTLEIIVTTSSKVLPPVSSNTDLTSEPTNTEQP 1019
866 TTESEVEFTTKGNNGNGPYESPSTH-----VKSSMDENSEFT----- 902
1020 TTLSTTSNITDITTSQPTGNDGNTSSNTPVPVPTVATSTLASABEDNKGSGHESASTS 1079
903 -----TSTAAS----- 908
1080 LKPSMGENGSLTSTTEIB---ATTSTPEAPSPAVSGTDTVTTEPTTRBQPTTLSTTSK 1136
909 -----TSTDENATIAITGSVEASSPIISSADET-----ATTITTA 946
1137 TNSLVATTQATNEN-GGKSPSTDLTSSLTGTSTASTSANSSELVTSVGTGAVASASND 1195
947 STSVI---EQPTNNNGGKAPSA-----TSSPSTTTTANNDSVITG-----TTSTN 989
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1196 QSHSTSVTMSNIVSNTPOTTLSQQVTSSTSPSTNTPIASTYDGSIIQHSWLYGLITL 1255
990 QSQSQSQSN-----SDTQOTTLSSQMTSSLVSLH--MLTTFDGSQSVIOHSTYLCGLITL 1042
1256 LSLFI 1260
1043 LSLFI 1047

RESULT 4
ABW01173
ID ABW01173 standard; protein; 1443 AA.
XX
AC ABW01173;
XX
DT 15-JAN-2004 (first entry)
XX
DE Candida albicans agglutinin-like sequence (ALS) 6 protein.
XX
KW Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide.
XX
OS Candida albicans.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by ACG"
XX
PN US2003124134-A1.
XX
PD 03-JUL-2003.
XX
PF 13-SEP-2002; 2002US-00245802.
XX
PR 19-NOV-1999; 99US-0166663P.
PR 18-NOV-2000; 2000US-00715876.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX
DR WFI; 2003-810971/76.
XX
DR N-PSDB; AAD62310.
XX
PT New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.
XX
PS Disclosure; Page 33-36; 65pp; English.
XX
CC The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) protein
XX
SQ Sequence 1443 AA;

Query Match 41.3%; Score 2680.5; DB 7; Length 1443;
Best Local Similarity 43.3%; Pred. No. 4.7e-130;
Matches 629; Conservative 215; Mismatches 387; Indels 223; Gaps 34;

Qy 8 LFVLYLSIASAKTITGVDFDSFNLSLTWSNAANYAKGCGYPTWNAVIGNSLDGTSANPGDTF 67
Db 9 LFFYCTITAMAKTISGVTFSNLSLTNTGNYPGGPGYPTTAVLGYSLDGTLASPGDTF 68
Qy 68 TLNMPVCVKYTTTSQTSVDLTADGVKATCOFYSGEFTTFTSLTCTVNDALKSISKAFGT 127
Db 69 TLVMPVCVKFTTQTSVDLTANGVKATCTFHAGEDFTTFSSMSCVYVNGLSNIRAFGT 128
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QY 2 LQOFTLLFLYLISAS--AKTINGVFDNSFNLSNAANYAFKPGCYPTWNAVLGWSLDGT 59
DQ 1 MKKLYLLYLLASFTTVISKEVGVNFQNSLIYTYRYEIEISLTANAOLEYALDGT 60
QY 60 SANPGDFTFLNMPGVKTYTTSQTSVDLPADGVKATCOFYSGEBEFTPTSTLTCTVNDALK 119
DQ 61 IASPGDFTFLVMPGVKTYTTSQTSVDLPADGVKATCOFYSGEBEFTPTSTLTCTVNDALK 120
QY 120 SSIAKACVTVTLPIAENVCGTSGSTLDESKCFETAGTNTVFNDDXKDISIDVEKSTVD 179
DQ 121 EDTSVFGSVILPIAENVCGTSGSTLDESKCFETAGTNTVFNDDXKDISIDVEKSTVD 180
QY 180 PSAYLYASRVMPLNKNVTLFVAPOCENGYSGTWGFSSNGDVAIDCSNHIHIGTKLN 239
DQ 181 AFGLVVSQRLNSMLDTNFMVWSTCFMGYSQGLGFTSNDDDFEIDCSSHVGITNEIN 240
QY 240 DWNYPVSSSESYTKTCSNGIQIKQNVPAQYRPFIDAYISATDVNOYTLAYTNDYFCA 299
DQ 241 DYSMPVSSVPDHTIRCTSRALYIEFKTIPAGYRPFVDAIVQIPTTEPFVKYTNERACV 300
QY 300 GSRLOSKEFTLWNT--GYKNSDAGSNGIIVATRTVTDSTTAVTLPNPSVDKTKIEI 358
DQ 301 NGIYTSIDPFSFQILYDEALATGADLVRTTSTVIGSITRTTLPFISRLQTKTILV 360
QY 359 LQPIPTTITTSYVGVTTSYLTKTAPIGBTATVIVDVPVHTTITVTSEMTGFTITTTTIRT 418
DQ 361 LEPIPTTITTSYVGVTTSYLTKTAPIGBTATVIVDVPVHTTITVTSEMTGFTITTTTIRT 420
QY 419 NPTSDIDTVVQVPLP-----NPTVSTTE 442
DQ 421 DDIDLVDIVIVKIPNPNFTIITQPYSGKYLTTETHEKPEPLGDSVILKEPHNPVTITE 480
QY 443 YWSQSFATTTTAPPGGTDVVIIEPPNHTVTTTEYWSQSFATTTTAPPGGTDVII 502
DQ 481 FYSESFAATTTITNYPEGDSVIVREPHNPVTTFEYSESFAATTTITNGPEGDSVIV 540
QY 503 REPNPVTVTTEYWSQSFATTTTAPPGGDSVILREPPNPTVTTFEYWSQSFATTTT 562
DQ 541 REPNPVTVTTFEYSESFAATTTITNGPEGDSVIVREPHNPVTTFEYSESFAATTTI 600
QY 563 TAPPGGDSVILREPPNHTVTTTEYWSQSFATTTTAPPGGTDVVIIEPPNHTVTTTE 622
DQ 601 TNGPEGDSVIVREPHNPVTTFEYSESFAATTTITNGPEGDSVILKEPHNPVTITK 660
QY 623 YWSQSFATTTTVPGGSDTVVIIEPPNPTVTTFEYWSQSFATTTTAPPGGTDVVI 682
DQ 661 FYSESFAATTTITNYPEGDSVIVREPHNPVTTFEYSESFAATTTITNGPEGDSVIV 720
QY 683 REPNPVTVTTFEYWSQSFATTTTAPPGGTDVVIIEPPNHTVTTTEYWSQSFATTTT 742
DQ 721 REPNPVTVTTFEYSESFAATTTITNYPEGDSVIVREPHNPVTTFEYSESFAATTT 780
QY 743 TAPPGGTDVVIIEPPNPTVTTFEYWSQSFATTTTAPPGGTDVVIIEPPNHTVTTTE 798
DQ 781 TNYPEGDSVIVREPHNPVTTFEYSESFAATTTITNYPEGDSVIVREPHNPVTTFEY 840
QY 799 ISTSNNDITSI-----IPS-----FSPR 816
DQ 841 IESSDPSNSSAQESSSSVQSFSTGADSTSSIVELSSRSIDIPSSSGLTSSSTVSYVD 900
QY 817 HYVNSTT-----SDLTSESSMNPPTSISDP--GMLLSSTT----- 851
DQ 901 SYSSSTSSSIASSYDSSSSSIESSTLSSSDRYSSISDITTFYDSSSSDLESTIYFS 960
QY 852 -----LVTESETTELICSDGKCEKRLSSSGIVNPNPSSSIVTSVTPAS 899
DQ 961 SSIDAQSHLVQSVNSISTQELISSSSSEESTSATDALVSSDASSILSDTSYFSS 1020
QY 900 TMSDLSLSDTGISATSSONVKSQSVVTTTSTVTTIQTTPNPLSSSVTLTQL-----SSI 955
DQ 1021 TISPDPPHTI--AGESDSQSISFITSITVIESSDSVSLTSDP--ESSPDSSSLRLNSDSSS 1078
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QY 956 PS-----VSESESKVTTFTSGNDQNGSQTHDSQSTSTBIKIVTTSSTKVLPP----- 1000
DQ 1079 PSTDQDILATSSSPSTLIKSSGREGSIGTILSESSDSIPTTFSTPYSPGSMSSRHYT 1138
QY 1001 -----VVSNT--DLTSEPTNTREQPTTLSTTNSITEDITTSQPTGDNCDNTSST 1049
DQ 1139 NSTETSVSDVSVSSVAGDETSESVSIVSESSVTSVASESVASESVASESV 1198
QY 1050 NPVPTVATSLASAREDNKSGHESASTSLKPMGNSGLTSTTEATEATTTSPTAPSP 1109
DQ 1199 TAVSDI--SDLYTSEVSTSDNSGMSPI--PSEQRS-----SIPIMSSDESSESR 1249
QY 1110 AVSSGTDVTTTEPTDREQPTTLST-----TSKTNSELVATQATNNGG 1153
DQ 1250 ESSSGTILSEENSDS--IPTFTSTRYVSPGMSRHRHTNSTETSTSVSDVSSVAGDETSE 1307
QY 1154 KPSP--TDLTSSLTGTASTANSSELVTSVGTGGAVASANDQSHSTSVTNSNS----- 1207
DQ 1308 SSVSIVSESVTSVASESVASESVAVSDISDLYTTSSEVVTSDNSGMS 1367
QY 1208 -----IVSNTPQ-----TTLSSQVTSSTSPSTWTFIATVDYDGSGLIQH 1245
DQ 1368 PIPSEQRSSIPVWSSDESSESSSGTILSEENSDSIPT--TFSTRYLSPGMSRHR 1425
QY 1246 ST 1247
DQ 1426 YT 1427

RESULT 7
ABW01169
ID ABW01169 standard; protein; 468 AA.
XX ABW01169;
AC ABW01169;
DT 15-JAN-2004 (first entry)
DE Candida albicans agglutinin-like sequence (ALS) 2 protein.
XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
XX candidiasis; vaccine; fungicide.
XX Candida albicans.
XX Key Location/Qualifiers
FT Misc-difference 41 /note= "Encoded by AAC"
XX US2003124134-A1.
XX 03-JUL-2003.
XX 13-SEP-2002; 2002US-00245802.
XX 19-NOV-1999; 99US-0166663P.
XX 18-NOV-2000; 2000US-00715876.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Edwards JB, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX WPI; 2003-810971/76.
XX N-PSDB; AAD62306.
XX New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.
XX Disclosure; Page 18-19; 65pp; English.
XX The present invention relates to a monoclonal antibody against an
CC agglutinin-like sequence (ALS)1 protein that specifically binds an
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CC epitope in an N-terminal domain and which inhibits adherence of Candida
CC albicans to endothelial cells. The invention is useful as vaccines for
CC treating and preventing disseminated candidiasis and for generating an
CC immune response capable of blocking adherence of the organism. The
CC invention is also useful in gene therapy. The present sequence is Candida
CC albicans agglutinin-like sequence (ALS) protein
XX

SQ Sequence 468 AA;

Query Match 30.7%; Score 1992.5; DB 7; Length 468;
Best Local Similarity 80.2%; Pred. No. 4.5e-95;
Matches 376; Conservative 33; Mismatches 59; Indels 1; Gaps 1;
QY 1 MLQOFTLLFLYLSIASAKTITGVDFNSLTWSNAAYAFKGPYPTWNAVLGWSLDGTS 60
DB 1 MLLQFLLLSLCVSVATAKVIITGVFNSFSLTWAGNYAYKGNRPRTWNAVLGWSLDGTS 60
QY 61 ANPGDTFTLNMPCVFKYKTTTSQTSVDLTADGVKATCQFYSGEPTFTSLTCTVNDALKS 120
DB 61 ANPGDTFTLNMPCVFKFTDQTSVDLTAEAGVKATCQFYSGEPTFTSLKCTVSNLTLS 120
QY 121 SIKAFGTVTLPFAFNVGTSSTLDESKCFAGTNTVTNDGDKDISIDVEPEKSTVDP 180
DB 121 SIKALGTVTLPISFNVGTSSTLDESSQCFKAGTNTVTNDGDKDISIDVDFEKTNEA 180
QY 181 SAYLYASRVMPSLNKKVTLFVAPQCENGYTSGMTGSSNGDVAIDCSNIHIGITKGLND 240
DB 181 SGYFIASRLPSINKSVITVAPQANGYTSGANGFIVLIGDTIDCSNVHVGITKGLND 240
QY 241 WNPVSSSEFSYTKTCTSNQIYKQNVAGYRPFIDAYISATDVNQYTLAYNDYTCAG 300
DB 241 WNPVSSDLSYNTKSTGISTGIYENVPAGYRPFIDVYTSVSGQR-QLRYNDYACVG 299
QY 301 SRLQSKPFTLRWTKYKNSDAGSNGIVIVATRTVTDSTTAVTLTPNPSVDKTKTIELQ 360
DB 300 SSLQSKPFLRLRGYNNSEANSNGFIVATRTVTDSTTAVTLTPNPSVDKTKTIELQ 359
QY 361 PIPTTTITTSYGVVTSYLTAKTAPIGETATVIVDVPYHTTTVTSEWGTITTTTTRNP 420
DB 360 PIPTTTITTSYGVVTSYLTAKTAPIGETATVIVDVPYHTTTVTSEWGTITTTTTRNP 419
QY 421 TDSIDTWWQVPLPNPTVSTTEYWSQSFAITTTTAPPGGTDVVIIEP 469
DB 420 TDSIDTWWQVPSNPFTVTTEYWSQSYATTTTAPPGGTDVVIIEP 468

RESULT 8
ABW01171
ID ABW01171 standard; protein; 469 AA.

XX AC ABW01171;
XX DT 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 4 protein.

DE Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide.

XX Candida albicans.

XX US2003124134-A1.

XX PD 03-JUL-2003.

XX PF 13-SEP-2002; 2002US-00245802.

XX PR 19-NOV-1999; 99US-0166663P.

XX PR 18-NOV-2000; 2000US-00715876.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;

XX WPI; 2003-810971/76.
DR N-PSDB; AAD62308.
XX
PT New monoclonal antibody against Candida albicans agglutinin-like sequence
PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
PT candidiasis, or to generate an immune response that blocks adherence of
PT the organism.
XX
PS Disclosure; Page 24-25; 65pp; English.

XX The present invention relates to a monoclonal antibody against an
XX agglutinin-like sequence (ALS) 1 protein that specifically binds an
XX epitope in an N-terminal domain and which inhibits adherence of Candida
XX albicans to endothelial cells. The invention is useful as vaccines for
XX treating and preventing disseminated candidiasis and for generating an
XX immune response capable of blocking adherence of the organism. The
XX invention is also useful in gene therapy. The present sequence is Candida
XX albicans agglutinin-like sequence (ALS) protein
XX

SQ Sequence 469 AA;

Query Match 28.0%; Score 1819; DB 7; Length 469;
Best Local Similarity 72.1%; Pred. No. 4.3e-86;
Matches 338; Conservative 48; Mismatches 83; Indels 0; Gaps 0;
QY 1 MLQOFTLLFLYLSIASAKTITGVDFNSLTWSNAAYAFKGPYPTWNAVLGWSLDGTS 60
DB 1 MLLQFLLLSLCVSVATAKVIITGVFNSFSLTWAGNYAYKGNRPRTWNAVLGWSLDGAT 60
QY 61 ANPGDTFTLNMPCVFKYKTTTSQTSVDLTADGVKATCQFYSGEPTFTSLTCTVNDALKS 120
DB 61 ASAGDTFTLDMPCVFKFTDQTSIDLVADGRTVATCNLSABEFTTFSVSCVTVTMTA 120
QY 121 SIKAFGTVTLPFAFNVGTSSTLDESKCFAGTNTVTNDGDKDISIDVEPEKSTVDP 180
DB 121 DTAKIGTVTLPFSFVSGSGSDVDLANSQCFTAGINTVTNFNDGDTISITVDPEKSTVAS 180
QY 181 SAYLYASRVMPSLNKKVTLFVAPQCENGYTSGMTGSSNGDVAIDCSNIHIGITKGLND 240
DB 181 SDRILLSRILPSLSQAVNLFLOECANGYTSGMTGFTAGTATDCSTVHVGISNGLND 240
QY 241 WNPVSSSEFSYTKTCTSNQIYKQNVAGYRPFIDAYISATDVNQYTLAYNDYTCAG 300
DB 241 WNPVSSSEFSYTKTCTSTSVLTQNVAPGYPFVDAYISATRVSSYTMQYTNVACVG 300
QY 301 SRLQSKPFTLRWTKYKNSDAGSNGIVIVATRTVTDSTTAVTLTPNPSVDKTKTIELQ 360
DB 301 AASVDSFTHWKGYSNSQAGSNGIIVVTRVTDSTTAVTLTPNPSVDKTKTIELQ 360
QY 361 PIPTTTITTSYGVVTSYLTAKTAPIGETATVIVDVPYHTTTVTSEWGTITTTTTRNP 420
DB 361 PIPTTTITTSYGVVTSYLTAKTAPIGETATVIVDVPYHTTTVTSEWGTITTTTTRNP 420
QY 421 TDSIDTWWQVPLPNPTVSTTEYWSQSFAITTTTAPPGGTDVVIIEP 469
DB 421 TDSIDTWWQVPSNPFTVTTEYWSQSYATTTTAPPGGTDVVIIEP 469

RESULT 9
ABW01176
ID ABW01176 standard; protein; 468 AA.

XX AC ABW01176;

XX DT 15-JAN-2004 (first entry)

XX Candida albicans agglutinin-like sequence (ALS) 9 protein.

XX Monoclonal antibody; agglutinin-like sequence; ALS; gene therapy;
KW candidiasis; vaccine; fungicide.

XX Candida albicans.

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XX PN US2003124134-A1.
XX PD 03-JUL-2003.
XX XX 13-SEP-2002; 2002US-00245802.
XX XX 19-NOV-1999; 99US-0166663P.
XX XX 18-NOV-2000; 2000US-00715876.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX XX Edwards JE, Filler SG, Sheppard DC, Ibrahim A, Fu Y;
XX WPI; 2003-810971/76.
XX DR N-PSDB; AAD62313.
XX XX
XX XX New monoclonal antibody against Candida albicans agglutinin-like sequence
XX PT 1 adhesin proteins, for use as a vaccine to treat or prevent disseminated
XX PT candidiasis, or to generate an immune response that blocks adherence of
XX PT the organism.
XX XX
XX PS Disclosure; Page 51-52; 65pp; English.
XX XX
XX CC The present invention relates to a monoclonal antibody against an
XX CC agglutinin-like sequence (ALS)1 protein that specifically binds an
XX CC epitope in an N-terminal domain and which inhibits adherence of Candida
XX CC albicans to endothelial cells. The invention is useful as vaccines for
XX CC treating and preventing disseminated candidiasis and for generating an
XX CC immune response capable of blocking adherence of the organism. The
XX CC invention is also useful in gene therapy. The present sequence is Candida
XX CC albicans agglutinin-like sequence (ALS) protein
XX XX
XX SQ Sequence 468 AA;
XX
Query Match 26.4%; Score 1717.5; DB 7; Length 468;
Best Local Similarity 68.7%; Pred. No. 7.7e-81;
Matches 322; Conservative 69; Mismatches 77; Indels 1; Gaps 1;
QY 1 LMQPTLLFLYLSTIASAKITGVFDSFNSLTWSNANAFKPGVPTWNAVLGSLDGT 60
DB 1 MLPQFILLFISLTWSTAKITGVFNSPDLATYRSVEYAYKGPETPTTNAVLYGLNSTT 60
QY 61 ANPGDTPLNWPCKYTTSTQSVDLTADGVKATCFYSGEETFTSLCTVNDALKS 120
DB 61 ADPGDTPLNWPCKYTTSTQSVDLTADGVSYATCDFNAGEEFTTFSLSCTVNSVS 120
QY 121 SIKAFGTVTLPAFNVGSGSTDLSDSKCTAGTNTVTFNDGDKDISIDVEFEKSTVDP 180
DB 121 YARVSGTVKLPITFNVGSGSVDLADSKCTAGKNTVTFMGDTKISTVDFDASVPSP 180
QY 181 SAYLYASRVMPSLNKVTLFLVAPQCENGYTGTMGFSSNGDVAIDCSNIHIGTKGLND 240
DB 181 SGYITSSRIIPSLNKLSSLFVVPQCENGYTGIMGFVASNG-ATIDCSNVNIGISKGLND 239
QY 241 WNPVSSSESYTKTCTENGQIKQNPAGVRPIDAYISATDVNQVTLAYTDYTCAG 300
DB 240 YNFPVSSSESYTKTCTSTSTVEFQNPAGVRPFVDAYISAENIDKVTLLTYANEYTCEN 299
QY 301 SRLQSKPTTLRTWGVKNSDAGSNGVIVATRTVTDSTTAVTLFPNPSVDKTKTIELIQ 360
DB 300 GNTVVDPTLLTYGVKNSDAGSDGVIVVTRVTDSTTAVTLFPNPSVDKTKTIELIQ 359
QY 361 PIPTTTITTSYGVVTSYLTKTAPIGETATVVDVPYHTTTVTSEWGTITTTTTRNP 420
DB 360 PIPTTTITTSYIGISTYETLTGTIGGTATVVDVPYHITATVNTFVTSITTTTNTNP 419
QY 421 TDSIDTVVQVPLNPMTVSTTHYWSQSFAITTVTAPGCGTDTVIREP 469
DB 420 TGSIDTVVQIPSPDPTTITTEFYGESFASITTTITNPDGTNSVIREP 468
XX
RESULT 10

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ADP87475
ID ADP87475 standard; protein; 1537 AA.
XX
AC ADP87475;
XX
DT 23-SEP-2004 (first entry)
XX
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.
XX
KW glucan synthase pathway; RNA expression; protein expression; YOL1 13W;
KW SKM1; YNR066C; YLR121C; YPS3; YHR209W; YKL161C; YFR030W; FLO1; YFR030W;
KW MET10; antifungal agent.
XX
OS Saccharomyces cerevisiae.
XX
PN W02004057033-A1.
XX
PD 08-JUL-2004.
XX
PF 17-DEC-2003; 2003WO-US040532.
XX
PR 19-DEC-2002; 2002US-00324035.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
XX
PI Phillips JW;
XX
WPI; 2004-500308/47.
XX
N-PSDB; ADP87474.
XX
PT Determining whether a molecule affects the function or activity of a
PT glucan synthase pathway in a S. cerevisiae cell by determining a change
PT in the RNA expression or protein expression in the cell of at least one
PT target polynucleotide.
XX
XX Disclosure; SEQ ID NO 17; 132pp; English.
XX
XX This invention relates to a novel method of determining if a molecule
XX affects the function or activity of a glucan synthase pathway in a
XX Saccharomyces cerevisiae cell which comprises determining if the RNA
XX expression or protein expression in the cell of at least one target
XX polynucleotide sequence is changed relative to the expression of said
XX target polynucleotide sequence in the absence of the molecule. The target
XX polynucleotide sequence is selected from the group consisting of YOL1 13W
XX (SKM1), YNR066C, YLR121C (YPS3), YHR209W, YKL161C, YFR030W (FLO1) and
XX YFR030W (MET10). The method is useful for determining whether a molecule
XX affects the function or activity of a glucan synthase pathway in an S
XX cerevisiae cell, possibly allowing development of antifungal agents for
XX use against a variety of pathogens. The present sequence is that of the
XX protein encoded by an S cerevisiae gene which may be used in the method
XX of the invention.
XX
XX SQ Sequence 1537 AA;
XX
Query Match 14.5%; Score 939; DB 8; Length 1537;
Best Local Similarity 25.8%; Pred. No. 6.4e-40;
Matches 414; Conservative 246; Mismatches 520; Indels 426; Gaps 84;
QY 2 LQOFTLLFLYLSTIASAKT-----ITGVFDSF-----NSLTWSNANAF----- 40
DB 10 LAVFTLLAL-TSVASGATEACLPAGQRKSGMNIIFYQYSLKDSSTSYNAAVMAYGASKT 68
QY 41 -----XGPGYPTW-----NAVLGSLD--G 58
DB 69 KLGSVGGQTDISIDNIPCVSSSGTFPCQSDSYGNCKGKMGACNSQGIAYWTDLFG 128
QY 59 TSANPGDFTFLNM-----PCVFKYTTSQ-----TSVD 85
DB 129 FYTTPTNV-TLEMTGYFLPQTGSGYTKFATVDDSDAILSVGATAFNCCAQQQPIITSN 187
QY 86 LTADGVK-----YATCQFYSGEETFTTSLCTVNDALKSSIKAFGT-----VTLP 131
DB 188 FTIDGKIPWGSLPPTNIEGTVMYAGYYPM-----KVVTYSNAVSWGTLPISVTP 238

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recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

xx SQ Sequence 1537 AA;

Query Match 14.5%; Score 939; DB 8; Length 1537;
 Best Local Similarity 25.8%; Pred. No. 6.4e-40;
 Matches 414; Conservative 246; Mismatches 520; Indels 426; Gaps 84;

QY 2 LQQTLLFLYLISAKT-----ITGVDFDSF-----NSLTWSNAANYAF----- 40
 DB 10 LAVFTLLAL-TSVASGATEACLPAGQRKSGMNIIFYVSLKDSSTYSNAAYMAYGASKT 68
 QY 41 -----KPGGPTW-----NAVLGHSLD--G 58
 DB 69 KLGSVGGQDIDISDYNIPCVSSSGTFPCQBDSDYGNMGCKMGACNSQGIAYWTDLFG 128
 QY 59 TSANPGDTFTLNM-----PCVPKYTSQ-----TSVD 85
 DB 129 FYTPTNV-TLEMTGYFLPOTGYSYTFKFAVDSDAISLSVGATFACCCAAQQPPISTN 187
 QY 86 LTADGVK-----YATCQFYSGBEFTFTLTCTVDNALKSSIKAFGT-----VTLF 131
 DB 188 FTIDGKPGWGLSPNIBGVYVYAGYYP-----KVYYSNAVSMGTLFISVTLF 238
 QY 132 IAFNVGGSTDLSDSKCFAGTNVTFPNDGDKDISIDVEFEKSTV-DPSAYLYASRM 190
 DB 239 -----DGTVDSDDFEG-----YVYSFDD-----DLSQSNCTVPDPNSYA-VSTTT 277
 QY 191 PSLNKVITLFAPOCENGYSGTGMPSSNGDVAIDCSNIHIGITKGLNDNYPVSSSEF 250
 DB 278 TTTEBWTGFTSTSTEMTGTGNGVPTDETVIIRPTTASTIITTEPNWSTFTSTST 337
 QY 251 SYTKTCTSGNIQIKYONVAGYRPPIDAYISATDVNOYTLAYTNDYTCAGSRLOSKPFTL 310
 DB 338 ELTTVGTNGVTRDEII-----VIRPTTATTAITTEPNWSTFTSTSTEL----- 384
 QY 311 RWTGVKNSDAGSNGI-----VIVATRTVTDSTAVTTL-PFNPVDKTKT----- 355
 DB 385 -----TTVGTNGLPTDETIIVIRPTTATTATTQPMNDTFTSTSTELTTVGTNGL 438
 QY 356 -----IELQIPPTTIT-----SYVGVTSLYLNKTA-----PIGETATVLDVDPYH 398
 DB 439 PTDETIIVIRPTTATTATTQPMNDTFTSTSTELTTVGTNGLPTDET-IIIRIPTT 497
 QY 399 TTT--TVTSEWTGII-----TTTTRTN--PTDSIDTVVQVPLPNPTVST-----EY 443
 DB 498 ATTAMTTQPNNDFTSTSTELTTVGTNGLPTD--ETIIIV--IRPTTATTATTQPN 552
 QY 444 WSQSFAIT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTEYWSQSFAIT-----TTV 490
 DB 553 WNDTFTSTSTEMTGTGNGLPTDETIIVIRPTTATTATTTEPNWSTFTSTSTEMT 612
 QY 491 TAPPG-GTDS--VIIREPPNHT--VTTEYWSQSFAIT-----TTVTAPPG-GTDS--VII 538
 DB 613 TGTNGLPTDETIIVIRPTTATTATTQPMNDTFTSTSTEMTGTGNGLPTDETIIV 672
 QY 539 REPPNHT--VTTEYWSQSFAIT-----TTVTAPPG-GTDS--VIIREPPNHT--VTTEY 587

DB 673 RTFTATTAMTTQPNNDFTSTSTELTTVGTGTLPTDETIIVIRPTTATTATTQPN 732
 QY 588 WSQSFAIT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTEYWSQSFAIT-----TTV 634
 DB 733 WNDTFTSTSTEMTGTGNGVPTDETVIIRPTTSEGLISTTTTEPWTGTFTSTSTEMT 792
 QY 635 T--GPPSGTDTVIIREPNNP--TVTTEYWSQSFAIT-----TTIAP-----POETDTVLI 682
 DB 793 TGTNGQPTDETVIIRPTTSEGLVTTTTEPWTGTFTSTSTEMTITGTNGVPTDETVI 852
 QY 683 REPPNHT--VTTEYWSQSFAIT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTEY 731
 DB 853 RTFTSEGLISTTTTEPWTGTFTSTSTEMTITGTNGQPTDETVIIRPTTSEGLISTTTEP 912
 QY 732 WSQSFAITTTVTAPPGTDT-----TVIIREPPNHT--VTTEYWSQSFAITTTVTAPP 782
 DB 913 WTGTFTSTSTEMTGTGNGVPTDETVIIRPTTSEGLISTTTTEPWTGTFTSTSTEMT 972
 QY 783 GGT-----DTVIIYSMSSSKI-----STSSNDITSIIPSPRP----- 816
 DB 973 TGTNGQPTDETVIIRPTTSEGLISTTTTEPWTGTFTSTSTEMTITGTNGQPTDETVI 1032
 QY 817 -----HYNSITSD-LSTFESSMNTPTSISSDGMLLSSTTLVTESETT-----TELICS 865
 DB 1033 RTFTSEGLVTTTTEPWTGTFTSTSTEMTGTGNGLPTDETVIIRPTTITAISSLSSSS 1092
 QY 866 DGKCEKRLSSSGIVTNP--DSNESSIVTSTVPTASTMSDLSSTDGISATSDNVKSG 923
 DB 1093 SGQITSSITSSRIIT-PFYPSNGTVISSSVSSSVTSSLTSSPVISSVSSITTS 1151
 QY 924 VSVTFTSVTTIOTTNPLSSSVTLQLSSIPSVSESESKVFTTSNGDNQSGTHDQST 983
 DB 1152 TSIFSSSKSV--IPTSSSTSGSESETSAGSVSSS-----SPISSESKSPYSSSS- 1204
 QY 984 STIEIVTTSST-----KVLPPVSVSNYDLTSTPTREQPTTLSTTS-----NSITE 1031
 DB 1205 ---LPLVTATTSQETASSLPAPT-----TKTSEQTLTVTSCSHVCTESISP 1252
 QY 1032 DITTSQPTGONGNTSSTN--PVPTVATSLAGASEDNKSGSHESASTSLKPSMGNSG 1089
 DB 1253 AIVSTATVTVSGVTTEYTTWCPISTTETTKQGTTEQTTKQTTVTVTSSCESDVCS 1312
 QY 1090 LTTSTEIATTTGTEAPSPAVSGTVDTEPTDTRQPTTLST-----SKTNSGLV 1142
 DB 1313 KTASPAIVSTSTATINGVTTEYTTWCPIST--TESRQQTLLVTVTSCSGVCSSETASPAI 1370
 QY 1143 ATT-----QATNENGCKSPSTDLSLTTGT--SASTSANSSELVTSQSV 1184
 DB 1371 VSTATATVNDVTVVYPTWRPQTANESVSSKMSATGETTTNTLAAETTTNTVAETITN 1430
 QY 1185 TGGA-----VASASNDQSHSTSV-----TNSNSIVSNTPTQTLSQ 1220
 DB 1431 TGAATKTVVTSLSRSNHAETQTASATDVIGHSSVSVSEIGTNTKSLTSSGLSTWSQ 1490
 QY 1221 VTSSSP-----STNTFIATYDGSIIQHSWLYGLITLLSLFI 1260
 DB 1491 PRSTPASSVMGYSTASLEISTYAGSANSLLAGSLSVFIASLLIAI 1536

RESULT 12
 AAR60562
 ID AAR60562 standard; protein; 1537 AA.
 XX AAR60562;
 AC AAR60562;
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 13-APR-1995 (first entry)
 XX Yeast 4.7 kb agglutination gene FLO1L.
 XX Yeast; agglutination; FLO1L.

OS Saccharomyces cerevisiae.

XX WO9419475-A2.
 XX
 PD 01-SEP-1994.
 XX
 XX 24-FEB-1994; 94WO-JP000290.
 XX
 XX 26-FEB-1993; 93JP-00038871.
 XX
 XX (SAPB) SAPPORO BREWERIES.
 PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
 XX
 XX Watari J, Takata Y, Ogawa M, Penttila M, Onnela M, Keraenen S;
 XX WPI; 1994-294338/36.
 DR N-PSDB; AAQ71390.
 XX
 XX New yeast agglutination genes and yeast contg. them - impart
 PT agglutination properties to facilitate removal from fermentation media.
 XX
 XX Disclosure; Page 43-48; 75pp; English.
 XX
 CC The agglutination gene is called FLO1. Saccharomyces cerevisiae includes
 CC an agglutination gene of 4.7 kb (FLO1L) and an agglutination gene of 2.6
 CC kb (FLO1S). FLO1L is the intact FLO1 gene on chromosome I, and FLO1S is
 CC the FLO1L gene with a portion of the ORF deleted in frame. FLO1L imparts
 CC a relatively strong agglutinative property to the host yeast into which
 CC it is introduced, while FLO1S imparts a weaker agglutinative property.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX
 XX Sequence 1537 AA;

Query Match 14.4%; Score 938; DB 2; Length 1537;
 Best Local Similarity 26.0%; Pred. No. 7.2e-40;
 Matches 417; Conservative 244; Mismatches 523; Indels 418; Gaps 85;
 2 LQQTLLFLYLISASAKT-----ITGVFDSF-----NSLTWSNAAYAF----- 40
 10 LAVFTLLAL-TSVASGATEACLPAGQRKSGNINFYQYSLKDSSTYSNAAYMAYGASKT 68
 41 -----KPGGYFTW-----NAVLGMSLD--G 58
 69 KLGSVGGOTDISIDYNIPCVSSSGTFPCQEDSYGNWCKGMGACNSQGIAYWSTDLFG 128
 59 TSANPGDTFTLNM-----PCVKYITSQ-----TSVD 85
 129 FYTTPTNV-TLEMTGYFLPQGTGYTFKFAVDSDSAILSVGGATFACCCAQOQPPITSTN 187
 86 LTADGVK-----YATQFYSGBEFTTFLCTVNDALKSSIKAFGT---VTLP 131
 188 FTIDGKPMWGSLLPNIEGTVMYAGYTPM-----KVYVSNVAVSGTLPISVTL 238
 132 IAFNVGGTSGSDLESKCEFTAGTNTVTFNDGDKDISIDVEFEKSTV-DPSAYLYASRM 190
 239 -----DGYTSDDFEG-----YVYSFDD-----DLSQSNCTVPDPSNYA-VSTTT 277
 191 PSLNKVYTLFVAPOCENGYSCTMGFSSNGSDVAIDCSNTHIGITKGLNDWNPVSSSEF 250
 278 TTTEPWTGTFSTSTSTMTVTGTNGVPTDETVIVIRTPPTASTIITTEPWNSTFTST 337
 251 SYTKTCSTNGIQIKQNVAPAGRYFPIDAYISATDVNQYTLAYNDYTCAGSRQKQPFLL 310
 338 ELTIVTGNGVRTDETL-----VIRPTATTAITTEPWNSTFTSTSTEL----- 384
 311 RWTGKNSDAGSNGI---VIVATRTVTDSTAVTTL-PNPNSVDKTKT----- 355
 385 -----TTVTGTNGLPTDETVIVIRTPPTATTAITTTQPNWDTFTSTSTMTVTGTNGL 438
 356 -----TEILOPIPTTIT-----SYGVTTSYLTAKA---PIGETATVIVDVPYH 398
 439 PTDETVIVIRTPPTATTAITTTQPNWDTFTSTSTMTVTGTNGLPTDET-IIVIRTPPT 497

QY 399 TTT--TVTSEWGTIT-----TTTRTN--PTDSIDTVVQVPLNPFT-VSTTEYWSQS 447
 DB 498 ATTAMTTTQPNWDTFTSTSTMTVTGTNGLPTDE-TIIVIRTPPTATTAMTTQPNWDT 556
 QY 448 PATT-----TTVTAPPG-GTD--TVIIRPPNHT--VTTEYWSQSFAIT-----TTVTAPP 494
 DB 557 FTSTSTMTVTGTNGLPTDETVIVIRTPPTATTATTEPWNSTFTSTSTELTTVTGTN 616
 QY 495 G-GTDS--VIIRPPNPT--VTTEYWSQSFAIT-----TTVTAPPG-GTDS--VIIRPP 542
 DB 617 GLPTDETVIVIRTPPTATTAMTTQPNWDTFTSTSTMTVTGTNGLPTDETVIVIRTPPT 676
 QY 543 NPT--VTTEYWSQSFAIT-----TTVTAPPG-GTDS--VIIRPPNHT--VTTEYWSQS 591
 DB 677 TATTAMTTTQPNWDTFTSTSTMTVTGTNGLPTDETVIVIRTPPTATTAMTTQPNWDT 736
 QY 592 YATT-----TTVTAPPG-GTD--TVIIRPPNHTV--TTTEYWSQSFAIT-----TTVT-- 635
 DB 737 FTSTSTMTVTGTNGLPTDETVIVIRTPPTSEGLISTTTTEPWTGTFTSTSTMTVTGTN 796
 QY 636 GPPSGTDTVIIRPPNP--TVTTEYWSQSFAIT-----TTITAP-----PGTDTVLIRPP 686
 DB 797 GQPTDETVIVIRTPPTSEGLISTTTTEPWTGTFTSTSTMTVTGTNGLPTDETVIVIRTPPT 856
 QY 687 NHTV--TTTEYWSQSFAIT-----TTVTAPPG-GTD--TVIIRPPNHTV--TTTEYWSQS 735
 DB 857 SEGLISTTTTEPWTGTFTSTSTMTVTGTNGLPTDETVIVIRTPPTSEGLISTTTTEPWTGT 916
 QY 736 YATT-----TTVTAPPG-GTD--TVIIRPPNHTV--TTTEYWSQSFAITTTVTAPPGT- 785
 DB 917 FTSTSTMTVTGTNGLPTDETVIVIRTPPTSEGLISTTTTEPWTGTFTSTSTMTVTGTN 976
 QY 786 -----DTVIIYSMSKKI-----STSSNDITSIIPSRP----- 816
 DB 977 GQPTDETVIVIRTPPTSEGLISTTTTEPWTGTFTSTSAEMTVTGTNGLPTDETVIVIRTPPT 1036
 QY 817 --HYNSTTSD-LSTPESSMNTPTSISSDGMLLGSTTLVTESETT-----TELICSDGKE 869
 DB 1037 SEGLVTTTTEPWTGTFTSTSTMTVTGTNGLPTDETVIVIRTPPTTAISSLSSSSSGQI 1096
 QY 870 CSRSLSSSGIVNTP--DSNESSIVTSTVPTASTMSDLSLSDGISATSDNYSKSGSVT 927
 DB 1097 TSISITSRPIIT--PFYPSNGTIVISSSVSSVTSLFTSSPVISSSVISSSTTTSTSTIF 1155
 QY 928 TETSVTTIQTENPLSSSVTSLTQSSIPSESESKVFTNGDNQSGTHDSQSSTSTEI 987
 DB 1156 SESSKSSV--IPTSSSTSGSSESETSSAGSVSS-----SFISESSKSPYSSSS---L 1205
 QY 988 EIVTTSST-----KVLPPVVSNTDLTSEPTNTRPQPTLSTTS-----NSITEDIYT 1035
 DB 1206 PLVTSATTSQETASSLPPATT-----TKTSEQTTLVTVTSCESHVCTESISPAIVS 1256
 QY 1036 SQPTGNGDNTSNTN--PVPTVATSTLASASEDNKSGSHESASTSLKPSMGNSGLTUS 1093
 DB 1257 TATVTVSGVTEYTTWCPISTTETTKQTKGTTEQTETTKQTTVTVTSSCESDVCSKTAS 1316
 QY 1094 TEATATTPTEAPSPAVSGTDTVTTEPTDTRPQPTLSTT-----SKTNSSELVATT- 1145
 DB 1317 PALVSTSTATINGVTEYTTWCPIST--TESRQOTTLVTVTSCESGVCSETASPAIVSTA 1374
 QY 1146 -----QATNENGKGPSTDLTSLTGT--SASTSANSSELVTVSGSVTGA 1188
 DB 1375 TATVNDVTVTVTPRQPTANEESVSKMNSATGETTNTLAATTTTNTVAAATITNTGAA 1434
 QY 1189 -----VASANDQSHSTSV-----TNSNSIVGNTPTLLSQOQVTS 1224
 DB 1435 ETKTVTVSSLSRSHAEOTASATDVIGHSSSVSVSETGNTKSLTSSGLSTMSQPRST 1494
 QY 1225 SP-----STNTFIASTYDGSIIQHSWLXGLITLLSLFI 1260
 DB 1495 PASSMWGYSTASLEISTYAGSANSLLAGSLGVFIASLLAL 1536

Db 949 SSVIPTSSSTSGSESETGSSASAS-----SSSSISSESPKSTYSSSLP-PVTSATTSQEI 1004
QY 952 LSSITPSVSESKVFTFTNGDQSGTHDSOSTSTEIETVTSSTKVLPPVVSNTDLTSE 1011
Db 1005 TSSLPPVTTTKT-----SEQTLLVTVTSCSHVCTESISSAIVSTAT 1046
QY 1012 PT---NTREOPTLLSTTSNITDIT-TSOPTGNDGNTSSTNPVPTVATSTILASASEED 1067
Db 1047 VTVSGATTEYTWCPISSTETITKQTTEKTKQTEQTTETTKQTTVVT---ISSCED 1103
QY 1068 --NKGSHGESASTSLKPSMGENGLTTSIEIAETTSPTPEAPVSSGVDVTEPTDTR 1125
Db 1104 VCSKTASPAIVSTSTATINGVTTEYTWCPISTTESKQQTLLVTVTSCSGVCSSET--- 1160
QY 1126 EQPTLLSTTKTNSSELVAT-----TOATNENGKSPSTDLTSSLTGTCSAST-----SA 1174
Db 1161 -SPAIVSTATATVNDVVTVVTSWRPQTNEQSVSSKMSATSETTTNIGAEYTTGTGA 1219
QY 1175 NSELVTSQSVT-----GGAVASASNDQSHSTSV-----TNSNSIVSNTPQTLLSQQVTS 1224
Db 1220 ETKTVTVTSISRFNHAETQTASATDVIGHSSVVSVSETGNTKSLTSSGLSTMSQQPRST 1279
QY 1225 -----SPSNWTFIASYDGGSIHQSTWLYGLITLLSLFI 1260
Db 1280 PASSMWGSSTASLEISTYAGSANSLLAGSLGVFIASLLAI 1321

RESULT 14
AAM24516
ID AAM24516 standard; protein; 5179 AA.
AC AAM24516;
XX
XX 12-OCT-2001 (first entry)
DE C899P predicted amino acid sequence.
KW Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
KW gene therapy; vaccine; colonic cancer.
OS Homo sapiens.
XX
XX W0200149716-A2.
XX 12-JUL-2001.
XX 29-DEC-2000; 2000WO-US035596.
XX 30-DEC-1999; 99US-00476296.
PR 10-JAN-2000; 2000US-00480321.
PR 15-FEB-2000; 2000US-00504629.
PR 06-MAR-2000; 2000US-00519444.
PR 19-MAY-2000; 2000US-00575251.
PR 29-JUN-2000; 2000US-00609448.
PR 28-AUG-2000; 2000US-00649811.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Lodes MJ, Secretist H, Benson DR, Meagher MJ, Stolk JA;
PI King GE, Wang T, Jiang Y;
XX
XX WPI; 2001-441847/47.
XX
XX Colon tumor associated proteins and nucleic acids useful for the
PT prevention, diagnosis and treatment of colonic cancer.
XX
XX Claim 2; Page 446-462; 472pp; English.
XX
XX The present invention describes colon tumour associated proteins (I) and
CC the polynucleotides (II) that encode them. (I) have cytostatic activity.
CC (I) and (II) may be used in gene therapy and vaccine production. (I) and
CC (II) may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate colon tumour associated protein (TCAP)

CC expression, such as colonic cancer. For example, (I) and (II) may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC TCAPs by expressing inactive proteins or to supplement the patients own
CC production of them. Additionally, (II) may be used to produce the TCAP
CC proteins, by inserting the nucleic acids into a host cell culturing the
CC cell to express the protein. (II) and its complementary sequences may
CC also be used as DNA probes in diagnostic polymerase chain reaction (PCR)
CC and hybridisation assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. (I) may also be used as antigens in the production
CC of antibodies against TCAPs and in assays to identify modulators of TCAP
CC expression and activity. Anti-(I) antibodies and antagonists may also be
CC used to down regulate TCAP expression and activity. The anti-(I)
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent
CC nucleotide and amino acid sequences given in the exemplification of the
CC present invention
XX
XX Sequence 5179 AA;

Query Match 11.1%; Score 721.5; DB 4; Length 5179;
Best Local Similarity 25.3%; Pred. No. 5.2e-28;
Matches 335; Conservative 158; Mismatches 554; Indels 279; Gaps 54;
QY 59 TSANPGDTFTLAMPKCVFKYTTTSQTSVDLTADGVKATCFQYSGEETFTSTLTCTVNDAL 118
Db 1647 TTTTPPTTTP8PP-----TTTTPSPPIITTTTPPTT-----TPSSPIITTTSPPT 1693
QY 119 KSSIKAFGTWLPFIAPNVGGTSGSDLEDSKCTAGTNTVTFNDGDKDISIDVEFKSTV 178
Db 1694 TTTTTPSPITTPSSPIITTTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTP 1747
QY 179 DP---SAYLYASRVMSLNKVT-----TLFVAPQCE-NGY-TSGTWGSSNGDVA 224
Db 1748 PPTTSSPLTTTLPSPSITPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTP 1807
QY 225 IDCSNIHIGITKGLNDWNPVSESEFSY-----TKTC-TSNGIQIKYQN-VPAGY 272
Db 1808 L-----IGDVCG-PGWAANI SCRATWYPDVIGQLGVCDVSVGLICKEDQKPGGV 1860
QY 273 RPFIDAYISATDVNQYTLAYTNDYTCAGSLRQSKPFTLRWTGYKNSDAGSNGIVVATTR 332
Db 1861 IEM-----APCLNVEINVQCC--ECVTQPTTMTTNTTENPTTPTTPTTPTTPTT 1907
QY 333 TVTSDTAVTTLFPNPSVDKTKIEILOPIPTTTTTSVGVTTSLTKTAPIG-ETATV 391
Db 1908 TPTPTPTGTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 1967
QY 392 IVDVPHVHTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 432
Db 1968 ---TPITTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 2024
QY 433 LPNPTVSTTEYWSQSFAITTTVTAPEGGTDVVIIEPPNHVTTTTEYWSQSFAITTTVTA 492
Db 2025 TPTPTGTQTP-TTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 2072
QY 493 PPGGTD-----SVIIEPPNPTVTTTEYWSQSFAITTTVTA---PGGTD-----S 535
Db 2073 TPTGTQTPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 2132
QY 536 VIIEPPNPTVTTTEYWSQSFAITTTVTA---PGGTDVVIIEPPNHVTTTTEYWSQS 592
Db 2133 TTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 2180
QY 593 ATTTTTPAPGGGTDVVIIEPPNHVTTTTEYWSQSFAITTTVTA---PGGTD-----T 643
Db 2181 -TTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 2226
QY 644 VIIEPPNPTVTTTEYWSQSFAITTTTAPPGGTDVLIIEPPNHVTTTTEYWSQSFAIT 703
Db 2227 TTVTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 2272

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OM protein - protein search, using sw model

Run on: September 8, 2005, 18:17:16 ; Search time 46 Seconds
(without alignments)
2044.735 Million cell updates/sec

Title: US-09-715-876-8
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4190.5	64.5	1191	4	US-09-248-796A-16243
2	3220	49.6	1060	4	US-09-248-796A-14123
3	2779	42.8	780	4	US-09-248-796A-16702
4	2297	35.4	646	4	US-09-248-796A-16701
5	2273	35.0	812	4	US-09-248-796A-16244
6	1994	30.7	511	4	US-09-248-796A-14125
7	1883	28.0	448	4	US-09-248-796A-14116
8	1816	28.0	426	4	US-09-248-796A-14114
9	1808.5	27.8	386	4	US-09-248-796A-14126
10	1634.5	25.2	522	4	US-09-248-796A-14121
11	1500.5	23.1	501	4	US-09-248-796A-14118
12	1206.5	18.6	300	4	US-09-248-796A-16245
13	1138	17.5	240	4	US-09-248-796A-14117
14	940	14.5	1537	1	US-08-325-267A-2
15	815	12.5	229	4	US-09-248-796A-16698
16	797	12.3	171	4	US-09-248-796A-14120
17	761	11.7	823	4	US-09-248-796A-16699
18	721.5	11.1	5179	4	US-09-538-092-1258
19	651	10.0	2137	3	US-09-134-001C-4463
20	648	10.0	176	4	US-09-248-796A-16696
21	640	9.9	232	4	US-09-248-796A-14122
22	583	9.0	154	4	US-09-248-796A-14119
23	553.5	8.5	2870	4	US-09-479-467A-15
24	553.5	8.5	3178	4	US-09-479-467A-4
25	521.5	8.0	1140	4	US-09-538-092-647
26	516	7.9	894	3	US-08-362-525-22
27	516	7.9	894	3	US-08-971-692-15

28	496	7.6	3892	4	US-09-328-352-5503	Sequence 5503, Ap
29	488	7.5	1721	3	US-08-928-361B-6	Sequence 6, Appli
30	488	7.5	1721	4	US-09-588-995A-6	Sequence 6, Appli
31	487	7.5	1721	3	US-08-700-651-5	Sequence 5, Appli
32	487	7.5	1837	3	US-08-928-361B-5	Sequence 5, Appli
33	487	7.5	1837	4	US-09-588-995A-5	Sequence 5, Appli
34	477	7.3	827	4	US-09-248-796A-17307	Sequence 17307, A
35	468.5	7.2	862	1	US-08-325-267A-4	Sequence 16703, A
36	449.5	6.9	529	4	US-09-948-796A-16703	Sequence 6513, Ap
37	441	6.8	1187	4	US-09-949-016-6513	Sequence 6930, Ap
38	440.5	6.8	2169	4	US-09-949-016-6930	Sequence 30227, A
39	433.5	6.7	2736	4	US-09-252-991A-30227	Sequence 330, App
40	415.5	6.4	1306	4	US-09-538-092-330	Sequence 6609, Ap
41	407.5	6.3	1938	4	US-09-949-016-6609	Sequence 5, Appli
42	404.5	6.2	2035	1	US-08-046-585-5	Sequence 5, Appli
43	404.5	6.2	2035	1	US-08-393-703-5	Sequence 5, Appli
44	404.5	6.2	2035	5	PCT-US93-11721-5	Sequence 5999, Ap
45	404	6.2	1747	4	US-09-134-000C-5999	

ALIGNMENTS

RESULT 1

US-09-248-796A-16243
; Sequence 16243, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Kelch Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16243
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16243

Query Match	64.5%	Score	4190.5	DB	4	Length	1191
Best Local Similarity	68.1%	Pred. No.	1.2e-230				
Matches	863	Conservative	89	Mismatches	195	Indels	121
Gaps	19						
Qy	1	MLQOFTLLFLYLSTASAKTITGVFDSFNSLTWSNAANYAFKPGYPTWNAVLSLDTGS	60				
Db	3	MLQOFTLLFLYLSTASAKTITGVFDSFNSLTWSNAANYAFKPGYPTWNAVLSLDTGS	62				
Qy	61	ANPGDTFLNMPVCVKYTTISQTSVDLADGVKYATCFYSGEBFTTSTLTCTVNDALKS	120				
Db	63	ANPGDTFLNMPCVFRVTTSQTSVDLADGVKYATCFYSGEBFTTSTLTCTVNDALKS	122				
Qy	121	SIKAFGTVTLPIANVNGTGSSTOLEDSKCFAGTNTVTENDGDKDISIDVEFEKSTVDP	180				
Db	123	SIKAFGTVTLPIANVNGTGSSTOLEDSKCFAGTNTVTENDGDKDISIDVEFEKSTVDP	182				
Qy	181	SAYLYASRVMSPLNKNVTLFVAPQENGYTSGTMGFSSNGDVAIDCSNIHIGITKGLND	240				
Db	183	SGYLYASRVMSPLNKNVTLFVAPQENGYTSGTMGFSSNGDVAIDCSNIHIGITKGLND	242				
Qy	241	WNYPVSSFSYTKTCTSNQIQIKNVPAGYRPFIDAYISATDVNQVTLAYTNDYTCAG	300				
Db	243	WNYPVSSFSYTKTCTSNQIQIKNVPAGYRPFIDAYISATDVNQVTLAYTNDYTCAG	302				
Qy	301	SRLOSKPFTLRWTGKNSDAGSNGIIVATRTTDSVTATVTLPPNSVDKTKTIELQ	360				
Db	303	SRLOSKPFTLRWTGKNSDAGSNGIIVATRTTDSVTATVTLPPNSVDKTKTIELQ	362				

QY 944 SSVTSLTOLSSIPS-----VSESESKVFTSNGDNQSGTHDSQSTS-----TEIEIV--- 990
Db 828 QSYATTTTITAPPGTDTVIIRPPNYVTITTEYWSQSYATTTTITAPPGTDTVIIRREP 887
QY 991 ---TTSSTKVLPPVSSNTDLTSEPTNT---REOPT-TLSTT---SNSITEDITTSQP 1038
Db 888 PNYVTITTEYWSQSYATTTTITAPPGTATVIIRPPNYVTITTEYWSQSYATTTTITGTP 947
QY 1039 TGDNGDNTSSNPVPTVATISLASASBEDNKGSHESASTSLKPSMGENSEGLTST--- 1094
Db 948 PGSTDTVIIRPPNPVTITTT-----EYWSQSYATTTTITAPPG-----TATVIIR 993
QY 1095 EIEATTTPTAPSPAVSSGTDVTPET---TDT---REOPTLSTTSKTNSELVATTOATN 1149
Db 994 EPPNTVTITTEYWSQSYATTTTITGPGGTDVIIRPPNPVTITTEYWS---LSYTRUSS 1051
QY 1150 ENGKKS 1155
Db 1052 ANAGRS 1057

RESULT 3
US-09-248-796A-16702
; Sequence 16702, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16702
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Candida albicans
; NAME/KEY: UNSURE
; LOCATION: (493)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-16702

Query Match 42.8%; Score 2779; DB 4; Length 780;
Best Local Similarity 64.0%; Pred. No. 1.8e-150;
Matches 550; Conservative 89; Mismatches 124; Indels 96; Gaps 8;
QY 1 MQQFTLLFLYLISASAKTITGVFDSFNSLTWSNAANYAFKPGGYPTWNAVGLWSLDGTS 60
Db 3 MQQFTLLFLYLISAPATAKAITGFNSIDLSLTWSNAGNAYFKPGGYPTWNAVGLWSLDGTS 62
QY 61 ANPGDTFLNMPGVKYYTTSQTSVDLTADGVKYATCQFYSGEEFTTFTSLCTVNDALKS 120
Db 63 ANPGDTFLNMPGVKFTASQKSVDLTADGVKYATCQFYSGEEFTTFTSLKCTVNNLRS 122
QY 121 STKAFGTVTLPAFNVGGTSGTDLRDSKCFAGTNTVTFNDGDKDISIDVPEKSTVDP 180
Db 123 STKALGTVTLPAFNVGGTSGVDLSDSKCFAGTNTVTFNDGSKLSIANNFELSTWDO 182
QY 181 SAYLYASRYMPSLNKVTTLFVAPQCENGYTSCTGMFSSNGDVAIDCSNIHIGITKGLND 240
Db 183 SGVLTTRPMPSLNKIATLYVAPQCENGYTSCTGMFSTSGDVAIDCSNVHIGISGVND 242
QY 241 WNPVSSSEFSYTKTCTSGNGIQKYNQVAPGRPFIDAYISATDYNQYTLAYNTDYTCAG 300
Db 243 WNPVTSSEFSYTKSCSFGISITQNVAPGRPFIDAYISPSDNNQYQLSKNDYTCVD 302
QY 301 SRLQSKPFTLRWTGYKNSDAGSNGIVVATTTTVDSTTAVTTLPENPSVDKTKTIEILQ 360

Db 303 DYMQHAPFTLRWTGYKNSDAGSNGIVVATTTTVDSTTAVTLPENPSVDKTKTIEILQ 362
QY 361 PIPPTTTTTSVGVTTSYLTKTAPIGETATVVDVPHYHTTTTSEWGTITTTTTRNP 420
Db 363 PIPPTTTTTSVGVTTSYLTKTAPIGETATVVDVPHYHTTTTSEWGTITTTTTRNP 422
QY 421 TDSIDTVDVQVPLPNPVTSTTEYWSQSFAITTTTITAPPGGTDTVIIRPPNHTVTTTYSW 480
Db 423 NDSIDTVDVQVPLPNPITTTITQFWSSESFISITTTITNSLKGTDSDVIIRPPNPTVTTTSEW 482
QY 481 SQSFATTTTITAPPGGTDSDVIIRPPNPTVTTTTEYWSQSFAITTTTITAPPGGTDSDVIIR 540
Db 483 SESYATTTITXGTLGTDSDVIIRPPNPTVTTTTEYWSQSFAITTTTITGTLGTDSDVIIR 542
QY 541 PPNTVTITTEYWSQSFAITTTTITAPPGGTDSDVIIRPPNHTVTTTTEYWSQSFAITTTTIT 600
Db 543 PHNPTVTITTFWSESYATTTITNKPGETSDVIIRPPNPTVTTTTEYWSQSFAITTTTIT 602
QY 601 PPGGTDTVIIRPPNHTVTTTTEYWSQSFAITTTTITGPPSGTDTVIIRPPNPTVTTTTEYW 660
Db 603 KPGGTDSDVIIRPPNPTVTTTTEYWSQSFAITTTTITGTLGTDSDVIIRPPNPTVTTTTEYW 651
QY 661 SQSYATTTTITAPPGGTDSDVIIRPPNHTVTTTTEYWSQSFAITTTTITAPPGGTDSDVIIR 719
Db 652 LEELSSTTAI-----ESSDSNISSAQESSSLVEQSSSIVGLSSSDIPLSS 698
QY 720 EPPNHTVTTTEYWSQSFAITTTTITAPPGGTDTVIIRPPNPTVTTTTEYWSQSFAITTTT 779
Db 699 DMPSSST-----GLTSS----- 712
QY 780 APPGTDTVIIRPPNHTVTTTSSNDITSIIPSPRPHYVNSTSDLSSTFSSSMNTPTS 839
Db 713 -----SSTVSSYDSDSS-----SSELSTFSSSESYSSISDITTFWDSS----- 752
QY 840 ISSDGMLLSSTTLVRESET 858
Db 753 -SSD-----LESTLITWSSS 766

RESULT 4
US-09-248-796A-16701
; Sequence 16701, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16701
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16701

Query Match 35.4%; Score 2297; DB 4; Length 646;
Best Local Similarity 69.0%; Pred. No. 4.2e-123;
Matches 428; Conservative 81; Mismatches 109; Indels 2; Gaps 1;
QY 8 LFLYLISASAKTITGVFDSFNSLTWSNAANYAFKPGGYPTWNAVGLWSLDGTSANPGDTF 67
Db 27 LFFYCTIAMAKTISGVFTSFNSLTVTNTGNTGYGPGGYPTWNAVGLWSLDGTLASPGDTF 86
QY 68 TLNMPGVKYYTTSQTSVDLTADGVKYATCQFYSGEEFTTFTSLCTVNDALKSISKARGT 127
Db 87 TLNMPGVKYYTTSQTSVDLTADGVKYATCQFYSGEEFTTFTSSMCSVNVNGLSSNIRAFGT 146


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Qy 128 VTLPIARNVGGTSSDLEDSKCFAGTNTVTFNDGDKDISIDVEFEKSTVDPSPAYLYAS 187
Db 147 VRLPIFNVGGTGSVNIQDSKCFAGTNTVTFDGHKISTVNVFFKTPQSSSLVYFA 206
Qy 188 RVMPSLNKKVTLFVAPOCENGYSGTWGFSSNGSDVAIDCSNIHIGITKGLNDMNPVSS 247
Db 207 RVIPSLDKLSLVASQCTAGYASGVLFGSATKDDVTDICSTIHVGITNGLNSWNPVSS 266
Qy 248 ESEFSYTKTCSNGIQIKQYNPAGYRPFIDAYI--SATDVNQYTLAYTNDYTCAGSLQS 305
Db 267 ESEFSYTKTCTPNSFIITYENVPAGYRPFIDYSYVKSATATNGENLNNTINYNCDWKGKN 326
Qy 306 KPFTLRWTGKNSDAGSNGIVIVATRTVDSSTAATVTLFPNPSVDKTKIEILQPIPT 365
Db 327 DPLIYFWTSYNSDAGSNGAAVVVTTVDSSTAATVTLFPDPVDKTKIEVIERPIPT 386
Qy 366 TITTSYGVVTSYLTKTAPIGETATVIVDPVYHTTTVTSEWGTITTTTTRNPTDSID 425
Db 387 TITTSYVGISLSTKTATIGGTAATVVVDVYHTTTTITSTWGTSTTSSTYTNPTDSID 446
Qy 426 TVVQVPLNPVTSTTEYWSQSFAATTTVTAPGGTDTVLIIRPPNHTVTTEYWSQSEA 485
Db 447 TVVQVPLNPVTSTTEYWSQSFAATTTVTAPGGTDTVLIIRPPNHTVTTEYWSQSEA 506
Qy 486 TTTTITVAPPCTDSVLIIRPPNPTVTTEYWSQSFAATTTVTAPGGTDSVLIIRPPNPT 545
Db 507 TTEVTNGPCTDSVLIIRPPNPTVTTEYWSQSFAATTTVTAPGGTDSVLIIRPPNPT 566
Qy 546 VTTTEYWSQSFAATTTVTAPGGTDSVLIIRPPNHTVTTEYWSQSFAATTTVTAPGGT 605
Db 567 VTTTEYWSQSFAATTTVTAPGGTDSVLIIRPPNHTVTTEYWSQSFAATTTVTAPGGT 626
Qy 606 DTVLIIRPPNHTVTTEYWS 625
Db 627 DSVIIRKEPHNPVTVTTEYWS 646

RESULT 5
US-09-248-796A-16244
; Sequence 16244, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16244
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16244

Query Match 35.0%; Score 2273; DB 4; Length 812;
Best Local Similarity 55.4%; Pred. No. 1.3e-121;
Matches 435; Conservative 130; Mismatches 218; Indels 2; Gaps 2;

Qy 7 LFLYLSTASAKTTGTGVPDSFNSLTWSNANYAKGPGYPTWNAVIGWSLDGTSANPGDT 66
Db 19 LLAFLTTVIS-KVETGVNQFNSLTWSYTYRAREYESTLTAKAQLWALDGTIASPGDT 77
Qy 67 FTLANPCVKYKTTSTOTSVDLTADGVKATCFYSGSEFTTPTSTLTCTVNDALKSKSIKAFG 126
Db 78 FTLVNCPVKYKWTYETSQLTANSIATCDPDAGEDTKFSSLSKCTVTDLTEDTSVFG 137
Qy 127 TVTLPFIARNVGGTSSDLEDSKCFAGTNTVTFNDGDKDISIDVEFEKSTVDPSPAYLYA 186
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Db 138 SVILPIAFNVGGSGSKTITDSKCFSSGYNTVTFDGNQNSTANFLPRRELAFGLVWS 197
Qy 187 SRVMPSLNKKVTLFVAPOCENGYSGTWGFSSNGSDVAIDCSNIHIGITKGLNDMNPVSS 246
Db 198 QRUSMSLDTWTFWMTSPCFMGYQLGKLGFTNDDDFEIDCSIIHVGITNEINDWSMPVSS 257
Qy 247 SESFSYTKTCSNGIQIKQYNPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSLQSK 306
Db 258 SVPFDDHTIRCTSRALYIEFKTIPAGYRPPVDAIVQIPTTEPPFVKYTNFACVNGIYTSI 317
Qy 307 PFTLRWT-GYKNSDAGSNGIVIVATRTVDSSTAATVTLFPNPSVDKTKIEILQPIPT 365
Db 318 PFTSFFSPILYDEALAIAGDLVTRTSTVIGSITRTTILPFIISRLQKTKILVLEPIPT 377
Qy 366 TITTSYGVVTSYLTKTAPIGETATVIVDPVYHTTTVTSEWGTITTTTTRNPTDSID 425
Db 378 TTVTSHHGDTWYTKAIGDATVDFIDVPOHTATLTLYWQESSTATTTFDDIDLVD 437
Qy 426 TVVQVPLNPVTSTTEYWSQSFAATTTVTAPGGTDTVLIIRPPNHTVTTEYWSQSEA 485
Db 438 TVIVKIPYENPTIITTFQWSGKYLATETHKBPPLGTDVLIIRKEPHNPVTVTTEYWSQSEA 497
Qy 486 TTTTITVAPPCTDSVLIIRPPNPTVTTEYWSQSFAATTTVTAPGGTDSVLIIRPPNPT 545
Db 498 TTTTITNPNPCTDSVLIIRKEPHNPVTVTTEYWSQSFAATTTTINNPGMDSVLIIRKEPHNP 557
Qy 546 VTTTEYWSQSFAATTTVTAPGGTDSVLIIRPPNHTVTTEYWSQSFAATTTVTAPGGT 605
Db 558 VTTTEYWSQSFAATTTTNGPCTDSVLIIRKEPHNPVTVTTEYWSQSFAATTTTNGPCT 617
Qy 606 DTVLIIRPPNHTVTTEYWSQSFAATTTVTAPGGTDTVLIIRPPNPTVTTEYWSQSEA 665
Db 618 DSVIVIREPHNPVTVTTEYWSQSFAATTTTNGPCTDSVLIIRKEPHNPVTVTTEYWSQSEA 677
Qy 666 TTTTITVAPPCTDSVLIIRPPNHTVTTEYWSQSFAATTTVTAPGGTDTVLIIRPPNPT 725
Db 678 TTTTITNPNPCTDSVLIIRKEPHNPVTVTTEYWSQSFAATTTTNGPCTDSVLIIRKEPHNP 737
Qy 726 VTTTEYWSQSFAATTTVTAPGGTDTVLIIRPPNPTVTTEYWSQSFAATTTVTAPGGT 785
Db 738 VTTTEYWSQSFAATTTTINNPGTDSVLIIRKEPHNPVTVTTEYWSQSFAATTTTINNPGT 797
Qy 786 DTVII 790
Db 798 DSVII 802

RESULT 6
US-09-248-796A-14125
; Sequence 14125, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14125
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14125

Query Match 30.7%; Score 1994; DB 4; Length 511;
Best Local Similarity 73.4%; Pred. No. 5.7e-106;
Matches 369; Conservative 52; Mismatches 82; Indels 0; Gaps 0;
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Qy	1	MLQOQFLFLXLYLSIASAKTIIGVDFDSFNSLFTWSNAANYAKPGCYPTWNAVLGWSLDGTS	60
Db	9	MLLQPLLXSLCVSAATAKVIIGIFDSFNSLFTWNAASYSYRGPANFTWTAIVIGWSLDGAT	68
Qy	61	ANPGDTFTLANMPCVKYKTTTSOTSDVLADGKVKATCOFYSGEBFTTFSTLTCTVNDALAKS	120
Db	69	ASAGDTFTLDMPCVKFKFTIDGTSIDLVADGETYATCNLSAEBFTTFSSVSCVTVTMTTA	128
Qy	121	STAKFGTVTLPFAFNVGGTSGSTOLEDSKCFAGTNTVFNDDGDKOISIDVBEKSTVDP	180
Db	129	DTKATGTVTLPFSFVSFGSGSDVLANSQCFAGINVTFNDDGTSLSATVDEKSTVAS	188
Qy	181	SAYLASRVMPSLNKVTTLFVAPOCENGYSGTGMGFSSNGDVAIDCSNIHIGITKGLND	240
Db	189	SDRILLRILPLSQAVSLFLPOECANGYTSGTGMGFSTAGTGATIDCSTVHVGISNGLND	248
Qy	241	WNPYVSSBSFSYTKTCTSNGLQIKQNPAGRYRPIDAYISATDVNQVLYLAYINDYTCAG	300
Db	249	WNPYISLESFSYTKTCTSTVLVTVQNPYAGRYRPFVDAYVSATRVSSYAMRYNIYACVG	308
Qy	301	SRLQSKPFLRWGTGYNKSDAGSNGIIVATRTVTDTSTTAVTTLFPNPSVDKTKTLEIQQ	360
Db	309	AAASVDSDFTHTWLGYSNSQAGSNGITIVVTRVTDTSTTAVTTLFPNSESDKTKLEIQQ	368
Qy	361	PIPTTTITTSYVGVTTSYLTKTAPIGETATVIVDVPHTTTTWTSEWGTITTTTTTRNP	420
Db	369	PIPTTTITTSYVGVTTSYLTKTAPIGETATVIVDVPHTTTTWTSEWGTITTTTTTRNP	428
Qy	421	TDSIDTVVVQVPLNPFTVSTTEYWSQSFATTTTVTAPPGGTDTVIVREPPNHTVTTTTEY	480
Db	429	TDSIDTVVVQVPLNPFTVTTTEYWSQSFATTTTVTAPPGGTDSVIVREPPNPVTTTTEY	488
Qy	481	SQSFATTTTVTAPPGGTDSVIVR	503
Db	489	SQSFATTTTVTAPPGGTDSMIVR	511

RESULT 7
US-09-248-796A-14116
Sequence 14116, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14116
LENGTH: 448
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-14116

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Db      120 ATTATTVAPPGTDTVLIREPPNHVTTTYWSQSAITTTTAPGGTDVLIREPPNH 179
Qy      545 TVTTYEWSQSYATTTTVTAPPGGSDSVIIREPPNHTVTTTYEWSQSYATTTTVTAPPG 604
Db      180 TVTTYEWSQSYATTTTVTAPPGGDSVIIREPPNHTVTTTYEWSQSYATTTTVTAPPG 239
Qy      605 TDTVIIREPPNHTVTTTYEWSQSFATTTTVTGPSGTDTVIIREPPNPTVTTTYEWSQS 664
Db      240 TDTVLIIREPPNHTVTTTYEWSQSAITTTTVTAPPGGTDVIIREPPNHTVTTTYEWSQS 299
Qy      665 ATTTTIAPPGETDVLIREPPNHTVTTTYEWSQSYATTTTVTAPPGGTDVLIREPPNH 724
Db      300 ATTTTVTAPPGGTDVIIREPPNHTVTTTYEWSQFAITTTTVTAPPGGTDVLIREPPNH 359
Qy      725 TVTTYEWSQSYATTTTVTAPPGGTDVIIREPPNPTVTTTYEWSQSFATTTTVTAPPG 784
Db      360 TVTTYEWSQSYATTTTVTGPPGETDVIIREPPNHTVTTTYEWSQSYATTTTVTAPPG 419
Qy      785 TDTVIIYESMSSKISTSSNDITSIIPSFSRPH 817
Db      420 YDTVIIIRETPNH---TVTNNEYS--KOLPQPH 447

RESULT 8
US-09-248-796A-14114
; Sequence 14114, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14114
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14114
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Query Match	28.0%;	Score 1816;	DB 4;	Length 426;
Best Local Similarity	79.3%;	Pred. No. 6.2e-96;		
Matches 341;	Conservative	33;	Mismatches 46;	Indels 10; Gaps 3;
QY	359	LQRIPTTIITTSYGVGTVSYLTXT--APIGETATVIUDVPVHTTTTTSBWTGTTTTTT	416	
DB	3	LSPPPS-----IGPNSKPTTNVIVPPGGTDSVIIREPPNPVTVTTEYWSQSFAITTTT	55	
QY	417	RTNPETDIDTVVQVQPLNPNTVSTTEYWSQSFAITTTTVPAPGGTDTVIIIREPPNHTVTT	476	
DB	56	VTAPPGGTDSVVIIEEP-PNPTVTTEYWSQSAYTTTIVTAPPGGTDVIIIREPPNYTVTT	114	
QY	477	TEYWSQSFAITTTTVPAPGGTDSVIIIREPPNPVTVTTEYWSQSFAITTTTVPAPGGTDSV	536	
DB	115	TEYWSQSAYTTTITGPPGGTDTVIIIREPPNPVTVTTEYWSQSAYTTTITVSPGGTDIV	174	
QY	537	IIREPPNPVTVTTEYWSQSAYTTTIVTAPPGGTDSVIIIREPPNHTVTTTEYWSQSAYTTT	596	
DB	175	IIREPPNPVTVTTEYWSQSFAITTTTVPAPGGTDSVIIIREPPNPVTVTTEYWSQSAYTTT	234	
QY	597	TVTAPPGGTDTVIIIREPPNHTVTTEYWSQSFAITTTTVPGGTDSVIIIREPPNPVTVT	656	
DB	235	TVTAPPGGTDSVIIIREPPNPVTVTTEYWSQSAYTTTIVTAPPGGTDSVIIIREPPNPVTVT	294	
QY	657	TEYWSQSAYTTTITVAPPGGTDTVIIIREPPNHTVTTEYWSQSAYTTTITVAPPGGTDTV	716	
DB	295	TEYWSQFVSITTTTVPAPGGTDSVIIIREPPNPVTVTTEYWSQSFAITTTVTPPGGTDSV	354	

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; PRIOR FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 14118
;; LENGTH: 501
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-09-248-796A-14118

Query Match 23.1%; Score 1500.5; DB 4; Length 501;
Best Local Similarity 55.8%; Pred. No. 7.4e-78;
Matches 298; Conservative 84; Mismatches 91; Indels 61; Gaps 7;

QY 396 PYHTTTTSEWTCGTTTTTTRNPTDSIDTVVQVPLPNTYSTTTEWMSQSFAITTTVT 455
DB 1 PYDPTVTTFWSESPASTTTVTNPPDGINSVIMPEY-NPTVTTFWFSEFAITTTVT 59
QY 456 APPGCTDVIIRPPNHTVTTFEWSQSFAITTTVTAPPDGTDSVIRPPNPTVTTFEY 515
DB 60 NPPDGRNSVIMPEYNTVTTFEWSFAITTTVTNPPDGTNSVIMPEYNTVTTFEY 119
QY 516 WSQSFAITTTVTAPPDGTDSVIRPPNPTVTTFEWSQSFAITTTVTAPPDGTDSVIR 575
DB 120 WSESPASTTTVTNPPDGTNSVIMPEYNTVTTFEWSFAITTTVTNPPDGTNSVIM 179
QY 576 EPPNHTVTTFEWSQSFAITTTVTAPPDGTDSVIRPPNHTVTTFEWSQSFAITTTVT 635
DB 180 EPPNHTVTTFEWSFAITTTVTNPPDGTNSVIMPEYNTVTTFEWSFAITTTVT 239
QY 636 GPPGCTDVIIRPPNPTVTTFEWSQSFAITTTVTAPPDGTDSVIRPPNHTVTTFEY 695
DB 240 NPPDGTNSVIMPEYNTVTTFEWSFAITTTVTNPPDGTNSVIMPEYNTVTTFEY 299
QY 696 WSQSFAITTTVTAPPDGTDSVIRPPNHTVTTFEWSQSFAITTTVTAPPDGTDSVIR 755
DB 300 WSESPASTTTVTNPPDGTNSVIMPEYNTVTTFEWSFAITTTVTNPPDGTNSVIM 359
QY 756 EPPNHTVTTFEWSQSFAITTTVTAPPDGTDSVIRPPNHTVTTFEWSFAITTTVT 813
DB 360 EPPNHTVTTFEWSFAITTTVTNPPDGTNSVIMPEYNTVTTFEWSFAITTTVT 419
QY 814 -----SRPHVNSTSDLSSTFESSMNTPTSISSDGMLLSSTLTVTSESTTELI 863
DB 420 SSFESTIPHSSEPHY-----SSDFSS-----DSFVTLISVTASSYDESS- 461
QY 864 CSDGKCEKRLSSSGIVNPDNESSIVTSTVPT-----ASTMSDSLSTDGISA 913
DB 462 -----IVSSFTPTLHLSSTYTWSSGLGSTRHFA 489

RESULT 12
US-09-248-796A-16245
; Sequence 16245, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208

;; SEQ ID NO 16245
;; LENGTH: 300
;; TYPE: PRT
;; ORGANISM: Candida albicans
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: (289)
;; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk
US-09-248-796A-16245

Query Match 18.6%; Score 1206.5; DB 4; Length 300;
Best Local Similarity 80.9%; Pred. No. 2.1e-61;
Matches 228; Conservative 15; Mismatches 38; Indels 1; Gaps 1;

QY 193 LNKVVTLLFVAPQCENGYTGTCMGFSSNGSDVAIDCSNIHIGITKGLNDMNPVSSBSFSY 252
DB 8 LTKQSLMWQPCQANGYTGSGMGFIVLTGTTIDCSNVHVGITKGLNDMNPVSSDLSY 67
QY 253 TKTCTSGNGIOIKYQNPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSLQSKPFTLRW 312
DB 68 NKTCSSTGISITTEMFPAGYRPFDFVTVLSDQNR-QLKYTNDYACVGSLSQSKPFLRL 126
QY 313 TGYKNSDAGSNGIVIAVTRTVDSTTATVTLFPNSVDKTKIILLQPIPTTTITSYV 372
DB 127 RGYNNSEANSNGFVIAVTRTVDSTTATVTLFPNSVDKTKIILLQPIPTTTITSYV 186
QY 373 GVTTSYLTKTAPIGETATVIVDPYHTTTVTSEWGTITTTTTRNPTDSIDTVVQV 432
DB 187 GVSTSYLTKTAPIGETATVIVDPYHTTTVTSEWGTITTTTTRNPTDSIDTVVQV 246
QY 433 LPNPTVTSTTEWMSQSFAITTTVTAPPDGTDSVIRPPNHTV 474
DB 247 LPNPTVTSTTEWMSQVATTTTITAHPGDGTDSVIRPPNHTV 288

RESULT 13

US-09-248-796A-14117
; Sequence 14117, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14117
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14117

Query Match 17.5%; Score 1138; DB 4; Length 240;
Best Local Similarity 98.7%; Pred. No. 1.2e-57;
Matches 231; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1027 NSITEDITTSQPTGNDGNDTSSTNPVPTVATSTLASAEDNKSGSHESASTSLKPSMGE 1086
DB 7 NPSREDITTSQPTGNDGNDTSSTNPVPTVATSTLASAEDNKSGSHESASTSLKPSMGE 66
QY 1087 NSGLTTSTTEIATTTSTPEAPSPAVSGGTDVTEPTDTRQPTTLSTTKNSSELVATQ 1146
DB 67 NSGLTTSTTEIATTTSTPEAPSPAVSGGTDVTEPTDTRQPTTLSTTKNSSELVATQ 126
QY 1147 ATNENGKSPSTDLTSSLTGTSASTSANGSELVTSVSGVTGAVASANDQSHSVTSNSN 1206
DB 127 ATNENGKSPSTDLTSSLTGTSASTSANGSELVTSVSGVTGAVASANDQSHSVTSNSN 186

QY 1207 SIVSNTPTQTLSQQVTSSTSTNTFFIASTYDGGSIIOHSTWLYGLITLLSLFI 1260
Db 187 SIVSNTPTQTLSQQVTSSTSTNTFFIASTYDGGSIIOHSTWLYGLITLLSLFI 240

RESULT 14

US-08-325-267A-2
; Sequence 2, Application US/08325267A
; Patent No. 5585271
; GENERAL INFORMATION:
; APPLICANT: WATARI, JUNJI
; APPLICANT: TAKATA, YOSHIHIRO
; APPLICANT: OGAWA, MASAHIRO
; APPLICANT: PENTTILA, MERJA
; APPLICANT: ONNELA, MAIJA-LEENA
; APPLICANT: KERANEN, SIRKKA
; TITLE OF INVENTION: YEAST AGGLUTINATION GENES AND YEAST
; TITLE OF INVENTION: CONTAINING THEM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,267A
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP PCT/JP94/00290
; FILING DATE: 24-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 38871/1993
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2589-023-0XPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1537 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-325-267A-2

Query Match 14.5%; Score 940; DB 1; Length 1537;
Best Local Similarity 26.0%; Pred. No. 3e-45;
Matches 417; Conservative 244; Mismatches 523; Indels 418; Gaps 85;

QY 2 LQQFTLLFLYLISASAKT-----ITGVDFSF-----NSLTWNAANYAF----- 40
Db 10 LAVFTLLAL-TSVASGATEACLPAGQRKSGMNFQYSLKDSSTYSNAAVMAYGYASKT 68
QY 41 -----KQGGPTW-----NAVILGSLD--G 58
Db 69 KLGSVGGQTDISIDYNIPCVSSSGTFPCQPDSDSYGNMGCKGMGACNSQGIAYWSTDLFG 128
QY 59 TSANPGDTFTLNM-----PCVKYTTTSQ-----TSVD 85
Db 129 FYTTPTNV-TLEMTGYFLPPQTGTYTFKATVDDSAILSVGGATAFNCAQQQPPITSTN 187

QY 86 LTADGVK-----YATCFYSGEBEFTTSTLTCTVNDALKSSIKAFGT-----VTLP 131
Db 188 FTIDGKIPWGGSLPPNIEGTVMYAGYYPM-----KVYISNAVSGWTLPISTVLP 238
QY 132 IAFNVGCTSSDLEDSKCFAGTNTVTFNDGDKOISIDVEFEKSTV-DPSAYLYASRVM 190
Db 239 -----DGTTVSDDFEG-----VYVSFDD-----DLQSQNCVTPDPSNVA-VSTTT 277
QY 191 PSLNKVTTILFVAPQCENGYTSGMTGFSSSNGDVDAIDCSNIHIGITKGLDNWNPVPSSESF 250
Db 278 TTTEPWTGFTST 337
QY 251 SYTKTCTNSGIIQIKYQNPAGYRPFIDAYISADVNQYTLAYNDVTCAGSRLOSKPFTL 310
Db 338 ELTTVTGTVGRVDETI-----VIRTPTTATTAITTEPWNSTSTSTSTSTSTSTST 384
QY 311 RWTGYNKSDAGSNGI---VIVATTRVTDSTTAVTTL-PNPSVDTKI----- 355
Db 385 -----TTVTGTNGLPFTDEIIIVIRPTTATTAMTTQPNNDTFTSTSTSTSTSTST 438
QY 356 -----IEILOPIPTTTIIT-----SYGVVTSYLTAKTA-----PIGETATVIVDPVYH 398
Db 439 PTDETIIVIRPTTATTAMTTQPNNDTFTSTSTSTSTSTSTSTSTSTSTSTSTSTST 497
QY 399 TTT--TVTSEWTGTTT-----TTTTRTN--PTDSIDTVVQVPLNPPT-VSTTEYWSQS 447
Db 498 ATTAMTTQPNNDTFTST 556
QY 448 FATT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTTEYWSQSFAAT-----TTVTAPP 494
Db 557 FTST 616
QY 495 G-GTDS--VIREPPNPT--VTTTEYWSQSFAAT-----TTVTAPPG-GTDS--VIREPP 542
Db 617 GLPTDETIIVIRPTTATTAMTTQPNNDTFTSTSTSTSTSTSTSTSTSTSTSTSTST 676
QY 543 NPT--VTTTEYWSQSFAAT-----TTVTAPPG-GTDS--VIREPPNHT--VTTTEYWSQS 591
Db 677 TATTAMTTQPNNDTFTST 736
QY 592 YATT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTTEYWSQSFAAT-----TTVT 635
Db 737 FTST 796
QY 636 GPPSGTDTVIREPPNPT--TVIIREPPNHT--VTTTEYWSQSFAAT-----TTVT 686
Db 797 GQPTDETVIRPTSEGLVTTTTTEPWTGFTSTSTSTSTSTSTSTSTSTSTSTSTST 856
QY 687 NHTV--TTEYWSQSFAAT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTTEYWSQS 735
Db 857 SEGLISTTTTEPWTGFTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 916
QY 736 YATT-----TTVTAPPG-GTD--TVIIREPPNHT--VTTTEYWSQSFAAT-----TTVT 785
Db 917 FTST 976
QY 786 -----DTVVIYESMSSSKI-----STSSNDITSIIIPFSRP----- 816
Db 977 GQPTDETVIRPTSEGLISTTTTEPWTGFTSTSTSTSTSTSTSTSTSTSTSTSTSTST 1036
QY 817 --HYVNSTTSD--LSTFESSSMWPTSISSDGMLLSSTTLVTESETT-----TELICDGKE 869
Db 1037 SEGLVTTTTTEPWTGFTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 1096
QY 870 CSRLSSSSGTVNTP--DSNESSIVTGTPTASTWMSDLSLSTSGISATSSDNVSKSGSVT 927
Db 1097 TSSITSRPIIT-PFVPSNGTSVISSSVSSSVTSLFTSSPVISSSVISSTTSTSTSI 1155
QY 928 TETSVTTIQTTPNPLSSSVTSLTQLSIPSVSSESKVFTFSTNGDNQSGTHDSQSTSTEI 987
Db 1156 SSSKSSV--IPTSSSTSGSSESTSGAGSVSSS---SFISSSESKSPYSSSS---L 1205
QY 988 EIVTTSST-----KVLPPVSSNNTDLTSEPTNREQPTLSTTS-----NSTEDITT 1035

Db	1206	PLVTSATISQETASSLPATT-----TKTSEQTLTVTSCESHVCTESISPAIVS	1256
Qy	1036	SQPTGDNQDNTSSN--PVPTVAITSLASEEHKNGSHESASTSLKPSMGENSEGLTTS	1093
Db	1257	TATVTVSGVTVTEYTWCPISITETTKQTGTEQTTETTKQTTVTVTSSCESDVCSTAS	1316
Qy	1094	TEIRATTTSPTEAPSPAVSSGTDVTBPTDRQOPTLSTT-----SKTNSELVATT-	1145
Db	1317	PAIVSTSTATINGVTTEYTWCPIST--TESRQQTLLVTVTSCESGVCSETASPAIVSTA	1374
Qy	1146	-----QATNENGKGSPTDLTSSLTTGT-SASTSANSSELVTSQVTTGA	1188
Db	1375	TATVNDVVVYPTWRPQTANESVSSKMSATGETTTWLAETTTNTVAAETITNTGAA	1434
Qy	1189	-----VASANDQSHSTSV-----TNSNSIVSNTPQTLLSQQVTS	1224
Db	1435	ETKTVTSSLSRNSHAETQTASATDVIGHSSSVSVSETGNTKLTSSGLSTMSQQRST	1494
Qy	1225	SP-----STNTFIASITYDGGSSIIQHSHTWLYGLITLLSLFI	1260
Db	1495	PASSVMGYSTASLEISTTAGSANSLLAGSLGSVFIASLLAI	1536

RESULT 15

US-09-248-796A-16698

; Sequence 16698, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 16698

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-16698

Query Match

Best Local Similarity

Matches 153; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

12.5%; Score 815; DB 4; Length 229;

75.7%; Pred. No. 3e-39;

Qy	1	MLQQFTLLFLYLISASAKTITGVFDSFNSLTWSNANYAFKPGPYTNNAVILGHSLDGTS	60
Db	9	MLLQFLLSLCVSATAKVITGVFNSFDSLTWTRAGNYAYKGNRPRTWNAVILGWSLDGTS	68
Qy	61	ANPGDFTLNMPGVFKYTTSTQTSVDLTADGVKYATCFQVSGEEFTTPTSLTCTVNDALKS	120
Db	69	ANPGDFTLNMPGVFKFTDQTSVDLTAGGVKIATCFQVSGEEFTTFFSLKCTVNTLTS	128
Qy	121	SIKAFGTVTLPIAFNVGGTGSSTDLSDSKCFAGTNTVTFNDDGDKDISIDVEFEKSTVDP	180
Db	129	SIKALGTVTLPISFNVGGTGSVDLENSQCQKAGTNTVTFNDDGDKKISIDVDDEKTNEDA	188
Qy	181	SAYLYASRVMPSLNKVTTLFVA	202
Db	189	SGYFIASRLIPSINKASITYVA	210

Search completed: September 8, 2005, 18:28:14

Job time : 51 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 18:26:58 ; Search time 184 Seconds

(without alignment)
2696.833 Million cell updates/sec

Title: US-09-715-876-8

Perfect score: 6495

Sequence: 1 MLOQFTLLFLYLSTASAKTI.....SIQHSTWLYGLITLLSLFI 1260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6465	99.5	1260	14	US-10-245-802-8
2	4204.5	64.7	1119	14	US-10-245-802-12
3	3938.5	60.6	1047	14	US-10-245-802-22
4	2680.5	41.3	1443	14	US-10-245-802-18
5	2584.5	39.8	1270	14	US-10-245-802-16
6	2452.5	37.8	2297	14	US-10-245-802-20
7	1992.5	30.7	468	14	US-10-245-802-10
8	1819	28.0	469	14	US-10-245-802-14
9	1717.5	26.4	468	14	US-10-245-802-24
10	939	14.5	1537	9	US-09-801-368-104
11	939	14.5	1537	15	US-10-369-493-1398

12	939	14.5	1537	17	US-10-324-035-17	Sequence 17, Appl
13	932.5	14.4	1322	9	US-09-801-368-114	Sequence 114, App
14	932.5	14.4	1322	15	US-10-369-493-1353	Sequence 1353, Ap
15	721.5	11.1	5179	9	US-09-922-217-1068	Sequence 1068, Ap
16	721.5	11.1	5179	9	US-09-833-263-1068	Sequence 1068, Ap
17	721.5	11.1	5179	13	US-10-025-380-1068	Sequence 1068, Ap
18	721.5	11.1	5179	16	US-10-734-564-121	Sequence 121, App
19	711	10.9	1075	9	US-09-801-368-111	Sequence 110, App
20	711	10.9	1075	15	US-10-369-493-22068	Sequence 22068, A
21	675.5	10.4	1367	9	US-09-801-368-108	Sequence 108, App
22	658	10.1	1831	15	US-10-282-122A-71033	Sequence 71033, A
23	658	10.1	1870	17	US-10-470-048B-268	Sequence 268, App
24	657.5	10.1	4262	17	US-10-704-781-4	Sequence 4, Appll
25	657.5	10.1	4493	17	US-10-704-781-3	Sequence 3, Appll
26	651	10.0	2137	18	US-10-724-972A-4951	Sequence 4951, Ap
27	646.5	10.0	2283	14	US-10-172-502-4	Sequence 4, Appll
28	646.5	10.0	2283	19	US-11-020-509-4	Sequence 4, Appll
29	640.5	9.9	2261	17	US-10-470-048B-60	Sequence 60, Appl
30	640.5	9.9	2344	9	US-09-815-242-12713	Sequence 12713, A
31	637.5	9.8	2271	15	US-10-282-122A-43924	Sequence 43924, A
32	624	9.6	800	14	US-10-029-386-32198	Sequence 32198, A
33	577.5	8.9	957	10	US-09-840-746-19	Sequence 19, Appl
34	577.5	8.9	1217	16	US-10-734-564-122	Sequence 122, App
35	574	8.8	1283	15	US-10-369-493-22616	Sequence 22616, A
36	553.5	8.5	1459	15	US-10-369-493-6418	Sequence 6418, Ap
37	547.5	8.4	1609	15	US-10-369-493-1535	Sequence 1535, Ap
38	545.5	8.4	957	9	US-09-922-217-1065	Sequence 1065, Ap
39	545.5	8.4	957	9	US-09-833-263-1065	Sequence 1065, Ap
40	545.5	8.4	957	13	US-10-025-380-1065	Sequence 1065, Ap
41	522.5	8.0	5877	14	US-10-142-515-11	Sequence 11, Appl
42	519.5	8.0	1794	10	US-09-965-738-299	Sequence 299, App
43	519.5	8.0	1799	10	US-09-965-738-149	Sequence 149, App
44	519.5	8.0	1821	10	US-09-965-738-82	Sequence 82, Appl
45	519.5	8.0	11721	10	US-09-965-738-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-10-245-802-8
; Sequence 8, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245.802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 1260
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-8

Query Match	99.5%	Score	6465;	DB	14;	Length	1260;
Best Local Similarity	99.6%	Pred. No.	0;				
Matches	1255;	Conservative	0;	Mismatches	5;	Indels	0;
						Gaps	0;
QY	1	MLOQFTLLFLYLSTASAKTIITGVDFSNLSLTSNAANYAFKPGYPTWNAVGLWSLDTGS	60				
Db	1	MLOQFTLLFLYLSTASAKTIITGVDFSNLSLTSNAANYAFKPGYPTWNAVGLWSLDTGS	60				
QY	61	ANPGDTFTLNNPCVFKYTTTSQTSVDLTADGVKYATCQFYSGBEFTTFTSLCTVNDALKS	120				
Db	61	ANPGDTFTLNNPCVFKYTTTSQTSVDLTADGVKYATCQFYSGBEFTTFTSLCTVNDALKS	120				
QY	121	SIKAFGTVTLPIAFNVGSGTSSTLDSKCFAGTAGTNTVTTFNDGDKDISIDVEFEKSTVDP	180				

121 SRAFGVTTLPIAFNVGGTSSDLEDSKCFCTAGTNTVTFNDGDKDISIDVPEKSTVDP 180
181 SAYLYASRVMPSLNKVTTLVFAQCENGYTSGTMGFSSNGDVDAIDCSNIHIGITKGLND 240
181 SAYLYASRVMPSLNKVTTLVFAQCENGYTSGTMGFSSNGDVDAIDCSNIHIGITKGLND 240
241 WNPVSESEFSYTKTCTSNIGIQIKYQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
241 WNPVSESEFSYTKTCTSNIGIQIKYQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
301 SRLQSKPFTLRWTKYKNSDAGSNGIIVATRTVTDSTTAVTLPNPNVSDKTKTILQ 360
301 SRSQSKPFTLRWTKYKNSDAGSNGIIVATRTVTDSTTAVTLPNPNVSDKTKTILQ 360
361 PIPTTTITTSYGVGVTTSYLTAKTAPIGETATVVDVPHHTTTTSEWGTGTTTTTTRNP 420
361 PIPTTTITTSYGVGVTTSYLTAKTAPIGETATVVDVPHHTTTTSEWGTGTTTTTTRNP 420
421 TDSIDTVVQVPLPNPTVSTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEY 480
421 TDSIDTVVQVPSNPVSTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEY 480
481 SQSFATTTTVPAGGTDVTVIIRPPNPTVTTTEYWSQSFATTTTVPAGGTDVTVIIR 540
481 SQSFATTTTVPAGGTDVTVIIRPPNPTVTTTEYWSQSFATTTTVPAGGTDVTVIIR 540
541 PPNPTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEYWSQSFATTTT 600
541 PPNPTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEYWSQSFATTTT 600
601 PPGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNPTVTT 660
601 PPGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNPTVTT 660
661 SQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIR 720
661 SQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIR 720
721 PPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNPTVTTTEYWSQSFATTTT 780
721 PPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNPTVTTTEYWSQSFATTTT 780
781 PPGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNPTVTT 840
781 PPGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNPTVTT 840
841 SSDGMLLSSTTLVTESETTTBLICSDGKCSRLSSSGIIVTNPDNNESSIVTSTVPTAST 900
841 SSDGMLLSSTTLVTESETTTBLICSDGKCSRLSSSGIIVTNPDNNESSIVTSTVPTAST 900
901 MSDLSSTDGLSATSNDNVKSGSVTETSTVTTIQTTPNPLSSSVTLQLSSIPSVSE 960
901 MSDLSSTDGLSATSNDNVKSGSVTETSTVTTIQTTPNPLSSSVTLQLSSIPSVSE 960
961 SESKVFTTNSGDNQSGHDSQSTTEIEIVTTSKVLPPVWSSNTDLTSEPTNTRQPT 1020
961 SESKVFTTNSGDNQSGHDSQSTTEIEIVTTSKVLPPVWSSNTDLTSEPTNTRQPT 1020
1021 TLTSTNSITDITTSQPTGNDGNTGSTNPVPTVATSTLASAEEKNKSGSHESASTSL 1080
1021 TLTSTNSITDITTSQPTGNDGNTGSTNPVPTVATSTLASAEEKNKSGSHESASTSL 1080
1081 KPSMGNSGLTSTTEIATTTSPTEAPSPAVSSGTDVTEPTDREOPTTLSTSKTNSE 1140
1081 KPSMGNSGLTSTTEIATTTSPTEAPSPAVSSGTDVTEPTDREOPTTLSTSKTNSE 1140
1141 LVATTQATNENGKSPSTDLTSSLTGTSASTSANSSELVTSVGTGAVASANDQSHST 1200
1141 SVATTQATNENGKSPSTDLTSSLTGTSASTSANSSELVTSVGTGAVASANDQSHST 1200
1201 SVTNSNGIVSNTPQTTLSQQVTSSSPSTNTFIATYDGSIIQHSWTWLYGLITLLSLFI 1260

1201 SVTNSNGIVSNTPQTTLSQQVTSSSPSTNTFIATYDGSIIQHSWTWLYGLITLLSLFI 1260
RESULT 2
US-10-245-802-12
; Sequence 12, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 12
; LENGTH: 1119
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-12

Query Match 64.7%; Score 4204.5; DB 14; Length 1119;
Best Local Similarity 64.9%; Pred. No. 1.7e-207;
Matches 844; Conservative 106; Mismatches 128; Indels 223; Gaps 18;

QY 1 MLOQPTLLFLYLSIASAKTITGVFDSFNSITWSNAAYAPKGPYPTWNAVLGWSLDGTS 60
DB 1 MLOQPTLLFLYLSIASAKTITGVFDSFNSITWSNAAYAPKGPYPTWNAVLGWSLDGTS 60
QY 61 ANPGDFTLNMPCVFXYTTSQTSVDLTADGVKYATCQFYSGBEFITFSTLTCTVNDALKS 120
DB 61 ANPGDFTLNMPCVFXYTTSQTSVDLTADGVKYATCQFYSGBEFITFSTLTCTVNDALKS 120
QY 121 SIKAFGTVTLPIAFNVGGTSSDLEDSKCFCTAGTNTVTFNDGDKDISIDVPEKSTVDP 180
DB 121 SIKAFGTVTLPIAFNVGGTSSDLEDSKCFCTAGTNTVTFNDGDKDISIDVPEKSTVDP 180
QY 181 SAYLYASRVMPSLNKVTTLVFAQCENGYTSGTMGFSSNGDVDAIDCSNIHIGITKGLND 240
DB 181 KGLVTSRVLPSLNKVTTLFVAPQCANGYTSCTMGFANTYGVQIDCSNIHIGITKGLND 240
QY 241 WNPVSESEFSYTKTCTSNIGIQIKYQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
DB 241 WNPVSESEFSYTKTCTSNIGIQIKYQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
QY 301 SRLQSKPFTLRWTKYKNSDAGSNGIIVATRTVTDSTTAVTLPNPNVSDKTKTILQ 360
DB 301 GYQORAPFTLRWTKYKNSDAGSNGIIVATRTVTDSTTAVTLPNPNVSDKTKTILQ 360
QY 361 PIPTTTITTSYGVGVTTSYLTAKTAPIGETATVVDVPHHTTTTSEWGTGTTTTTTRNP 420
DB 361 PIPTTTITTSYGVGVTTSYLTAKTAPIGETATVVDVPHHTTTTSEWGTGTTTTTTRNP 420
QY 421 TDSIDTVVQVPLPNPTVSTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEY 480
DB 421 TDSIDTVVQVPSNPVSTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEY 480
QY 481 SQSFATTTTVPAGGTDVTVIIRPPNPTVTTTEYWSQSFATTTTVPAGGTDVTVIIR 540
DB 481 SESYTTTSTTAPAGGTDVTVIIRPPNPTVTTTEYWSQSFATTTTVPAGGTDVTVIIR 540
QY 541 PPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEYWSQSFATTTT 600
DB 541 PPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEYWSQSFATTTT 600
QY 601 PPGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNPTVTT 660
DB 601 PPGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIRPPNPTVTT 660
QY 661 SQSFATTTTVPAGGTDVTVIIRPPNHTVTTTEYWSQSFATTTTVPAGGTDVTVIIR 684

Db 661 SOSYATTTTITAPPGTDTVLIREPPNHTVTTTYSQSFAATTTTATPPGDTVLIRE 720
Qy 685 PPNHTVTTTYSQSAYATTTTATPPGDTVLIREPPNHTVTTTYSQSAYATTTTATPPGDTVLIRE 744
Db 721 PPNHTVTTTYSQSAYATTTTATPPGDTVLIREPPNHTVTTTYSQSAYATTTTATPPGDTVLIRE 780
Qy 745 PPGGDTVLIREPPNHTVTTTYSQSAYATTTTATPPGDTVLIREPPNHTVTTTYSQSAYATTTTATPPGDTVLIRE 804
Db 781 PPGGDTVLIREPPNHTVTTTYSQSAYATTTTATPPGDTVLIREPPNHTVTTTYSQSAYATTTTATPPGDTVLIRE 836
Qy 805 DITSIIIPSPRPHYVNSSTDLSTFESSMNTPTSISSDGMLLSSTTLVTESETTELIC 864
Db 837 -----SFSRPHYVNTHT-----LWSITWVETKTIETSC 866
Qy 865 SDGKECRLSSSGIVTNPDSNEISVTSVPTASTMSDLSSTDGISATSSDNVSKGV 924
Db 867 EGDGKCSWVSSTRIVTIPNNIETPMVNTVDSTTETS-QSPGI-----FSESgv 918
Qy 925 SVTTETS-VTTIQTTPNPLSSSVTSLTQSLIPSVSESKVTFTSNGDNQSGTHDSQST 983
Db 919 SVETESSVTTAQTN-----PSVPTTESEVWFTTKGNNGPYESPST 961
Qy 984 STEIEIVTTSKVLPPVVSSNTDLTSEPTNTREQPTTLSTTSNSITEDITTSOPTQDNG 1043
Db 962 N-----VKSSMDENSEFT----- 974
Qy 1044 DNTSSTNPVPTVATSLASAEEDKSGSHESASTSLKPSMGENSEGLTSTEIE---ATT 1100
Db 975 -----TSTAAS-----TSTDIENTIAT 992
Qy 1101 TSPTREAPVAVSGGDTVTTEPTDTREQPTTLSTTSKTNSELVATTOATNEN-GGKSPSTD 1159
Db 993 TGSVERASSPILSSSADET-----TVTITAEISTVI---EQPTNNGGKAPSA- 1038
Qy 1160 LTSSLTTCSTASANSBLVTSVGTGAVASANDQSHSTSVTNSNSIVSNTPQTLSQ 1219
Db 1039 -----TSSPSITTTANNDVITG-----TSTNSQSOSQYN-----SDTQQTLSQ 1080
Qy 1220 QVTSSSPNTFIASTYDGSIIQHSWLGITLILSLFI 1260
Db 1081 QMTSSLVSLH--MLTTFDGSVIOHSTWLCGLITLILSLFI 1119

RESULT 3
US-10-245-802-22
; Sequence 22, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; FILE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-22

Query Match 60.6%; Score 3938.5; DB 14; Length 1047;
Best Local Similarity 63.7%; Pred. No. 7.2e-194;
Matches 806; Conservative 116; Mismatches 120; Indels 223; Gaps 18;

Qy 1 MLQQTFLFLYLISASAKITGVDPFSNLSWTNSNAANYAKPGPYPTNAVLGWSLDGTS 60
Db 1 MLQQTFLLLIYLVSATAKITGVDPFSNLSWTNSNAANYHYKPGPYPTNAVLGWSLDGTS 60

Qy 61 ANPGDTFLNMPCVFKYKTTSTQTSVDLTADGVKATCOFYSGEBFTTSTLTCTVNDALKS 120
Db 61 ASPGDTFLNMPCVFKFTTSTQTSVDLTADGVKATCOFQAGEBFTTSTLTCTVNSLTLP 120
Qy 121 SIKAPGTVTLPIAPNVTGSGTSDLEDSCFTACTNTVTFNDGDKDISIDVPEKSTVDP 180
Db 121 SIKALGTVTLPIAPNVTGSGTSDLEDSCFTACTNTVTFNDGDKDISIDVPEKSTVDP 180
Qy 181 SAYLYASRVMPSLMKVTTFLFVAPQCENGYTSGTWFSSSNGSDVAIDCSNIHIGITKGLND 240
Db 181 KGYLTSRVIPSLMKVSTLFLVAPQCANGYTSWTGFANTYGDVQIDCSNIHVGITKGLND 240
Qy 241 WNPVSVSESYTKTCTSNIGIQIKYQNVAPAGRPFDIAYISATDVNQYTLAYTDNYTCAG 300
Db 241 YNPVSVSESYTKTCTSNIGIFITYKNVPAGRPFDVDAIYISATDVNSYTLISYANETCAG 300
Qy 301 SRLQSKPTLRWTKYKNSDAGSNGIVVATRTVTDSTTATVTLPPNPSVDKTKTIRLQ 360
Db 301 GYTORAPFTLRKYTGYSRNSDAGSNGIVVATRTVTDSTTATVTLPPNPDNRDKTKIIRLK 360
Qy 361 PIPPTITTSVGVVTSYLTAKTAPIGETATVIVDVPYHTTITVTSEWTGTTTTTTRNP 420
Db 361 PIPPTITTSVGVVTSYLTAKTAPIGETATVIVDIPYHTTITVTSKYTGTTTSTTHNP 420
Qy 421 TDSIDTVVQVPLPNPTVSTTEYWSQSFAATTTTATPPGDTVLIREPPNHTVTTTETW 480
Db 421 TDSIDTVIVQVPSNPVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHTVTTTETW 480
Qy 481 SQSFATTTTATPPGDTSVLIIRPPNPTVTTTTEYWSQSFAATTTTATPPGDTSVLIIR 540
Db 481 SESYTTTSTTATPPGDTSVLIIRPPNPTVTTTTEYWSQSFAATTTTATPPGDTSVLIIR 540
Qy 541 PPNHTVTTTTEYWSQSAYATTTTATPPGDTVLIREPPNHTVTTTTEYWSQSAYATTTT 600
Db 541 PPNHTVTTTTEYWSQSAYATTTTATPPGDTVLIREPPNHTVTTTTEYWSQSAYATTTT 600
Qy 601 PPGGDTVLIREPPNHTVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHTVTTTETW 660
Db 601 PPGGDTVLIREPPNHTVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHTVTTTETW 660
Qy 661 SQSFATTTTATPPGDTVLIREPPNHTVTTTTEYWSQSAYATTTTATPPGDTSVLIIR 720
Db 625 SQSFATTTTATPPGDTVLIREPPNHTVTTTTEYWSQSAYATTTTATPPGDTSVLIIR 684
Qy 721 PPNHTVTTTTEYWSQSAYATTTTATPPGDTVLIREPPNHTVTTTTEYWSQSAYATTTT 780
Db 685 PPNHTVTTTTEYWSQSAYATTTTATPPGDTVLIREPPNHTVTTTTEYWSQSAYATTTT 744
Qy 781 PPGGDTVLIREPPNHTVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHTVTTTETW 840
Db 745 PPGGDTVLIREPPNHTVTTTTEYWSQSFAATTTTATPPGDTVLIREPPNHTVTTTETW 776
Qy 841 SSDGMLLSSTTLVTESETTELICSDGKESRLLSSSGIVTNPDSNEISVTSVPTAST 900
Db 777 -----LYSTTVVETKTIETSCGDKGCSYVSTRIVTIPNNIETPMVNTVDSTT 830
Qy 901 MSDLSLSTDGISATSSDNVSKSGVSVTETS-VTTIQTTPNPLSSSVTSLAQSLSPSVS 959
Db 831 ESTS-QSPGI-----FSESgvSVTETS-VTTIQTTPNPLSSSVTSLAQSLSPSVS 865
Qy 960 ESKSVTFTSNGDNQSGTHDSQSTSTEIEIVTTSKVLPPVNSNTDLTSEPTNTREQ 1019
Db 866 TTESEVFTTKGNNGPYESPSTH-----VKSSMDENSEFT----- 902
Qy 1020 TTLSTTSNITEDITTSOPTQDNGDNTSTNPVPTVATSLASAEEDKSGSHESASTS 1079
Db 903 -----TSTAAS----- 908
Qy 1080 LKPSMGENSEGLTSTEIE---ATTSPTEAPSPVSGDTVTTEPTDTREQPTTLSTTSK 1136
Db 909 -----TSTDIENTIATGSEASPISSADET-----TITTTAE 946
Qy 1137 TNSBLVATTOATNEN-GGKSPSTDLTSSLTTCSTASANSBLVTSVGTGAVASAND 1195

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Db      947 STSVI-----EQPTNNNGGKAPSA-----TSSPSTTTTANNDSDVITG-----TTSTN 989
Qy      1196 QSHSTSVTNSINVSNTPTQTLTSSQVTSVSSPSTNTFTASTYDGSGLIIOHSTWLYGLITL 1255
Db      990 QSQSQSQSN-----SDTQQTLSQOMTSSLSLH--MLATTFDGSGLIIOHSTYLCGLITL 1042
Qy      1256 LSLFI 1260
Db      1043 LSLFI 1047

RESULT 4
US-10-245-802-18
; Sequence 18, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-18

Query Match      41.3%; Score 2680.5; DB 14; Length 1443;
Best Local Similarity 43.3%; Pred. No. 3.9e-129;
Matches 629; Conservative 215; Mismatches 387; Indels 223; Gaps 34;

Qy      8 LFLVLSASAKITGVFDSFNSLTWSNAANYAFKPGYPTWNAVLGWSLDGTSAKPGDTF 67
Db      9 LFFCTIAMAKITSGVTSFNSLTWYTGNYPGYGPYTYAVLGYSLDGTLASPGDTF 68
Qy      68 TLNMPGVFKYTTQTSVDLTADGVKATCOFYSGEEFTTFTSLTCTVNDALKSIKAGT 127
Db      69 TLNMPGVFKYTTQTSVDLTANGVKATCTFHAGEDFTTFSSMVCVNVNGLSSNIRAGT 128
Qy      128 VTLPIAFNVGTSSTLEDSKCTAGTNTVTFNDGKDISIDVEPEKSTVDPSAYLAS 187
Db      129 VRLPISFNVGTSNVIQDSKCTAGTNTVTFDGDHKISTTVNFPKTPQSSSLVYFA 188
Qy      188 RVMPSLNKTTLFVAPOCENGYTSGTGMFGSSNGDVAIDCSNIHIGITKGLNDWNPVSS 247
Db      189 RVIFSLDKLSLVASQCTAGYAGVGLGFAKDDVDIDCSTIHVGLITGLNSYNMPVSS 248
Qy      248 ESFSYTKTCTSNIGIQYQNVAGYRPFIDAYI--SATDVNQYTLAVTNDYTCAGSLQS 305
Db      249 ESFSYTKTCTSPNFIITVENVPAGYRPFIDSYVVKSAATANGFNALNTIYNCMGKGN 308
Qy      306 KPFTLRWTKYKNSDAGSNGIVIVATRTVDTSTTAVTTLNPNPSVDKTKIEILQPIPTT 365
Db      309 DPLIFYFTSYTNSDAGSNGAAVVVTVTVDSTTAITLPPDPFDVKTKIEVIEPIPTT 368
Qy      366 TITTSYGVGTVTSYLTAKPIGICATATVVDVPHYTTTTSWETGTTTTTTRTNPTDSID 425
Db      369 TITTSYGVGISLSTKATIGGTATVVDVPHYHTTTTITSYTGSAATTSSTYNPTDSID 428
Qy      426 TVVQVQLPNPTVSTTEYWSQSFATTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSPA 485
Db      429 TVVQVPSNPVTVTTQFYSGSVPTTETVTTGPGQSDSVIIKEPHNPVTVTTTEYWSQSPA 488
Qy      486 TTTTVTAPPGGTDVSVIIREPPNPTVTTTEYWSQSFATTTVTAPPGGTDVSVIIREPPNPT 545
Db      489 TTTVTNNPEGTDVSVIIKEPHNPVTVTTTEYWSQSFATTTVTNNPEGTDVSVIIREPPNPT 548
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Qy      546 VTTEYWSQSFATTTVTAPPGGTDVSVIIREPPNHTVTTTEYWSQSFATTTVTAPPGGT 605
Db      549 VTTEYWSQSFATTTVTNNPEGTDVSVIIREPPNPTVTTTEYWSQSFATTTVTNNPEGT 608
Qy      606 DTVILIREPPNHTVTTTEYWSQSFATTTVTGPGGTDVTVIIREP----- 649
Db      609 DSVIVIREPPNPTVTTTEYWSQSFATTTTTPGLGTDVSVIHDPLESSSSTAIESSDSN 668
Qy      650 -----PNPTVTTEYWS-----QSYATTTT 669
Db      669 ISSAQESSSSVEQSLTSADETSSIVELSSRDIPSSSIGLTSSESTVSSYDSSSSIS 728
Qy      670 ITAPPGGTDVTVIIREPPNHTVTTTEYWSQSFATTT-----TVTAPPGETD 714
Db      729 ESSIASYDSSSSIESSTLSSDRCSISDTSFYDSSSDLESTSIYSSSIDAQS 788
Qy      715 TVILIREPPNHTVTTTEYWSQSFATTTVTAPPGGTDVTVIIREP-----PNPTV 762
Db      789 SHLVQSVNSISSTQBELSSSSSEESTF-----ATDALVSSDASSILSDTSYSPSTI 843
Qy      763 TTTEYW-----SQSFATTT-----TVTAPPGT-DTVIIESSSSSIS 802
Db      844 SSDDDFPHIAGESDLSISFITSTVEISSDSVSLTSDPASSFDSSSLNSDSSSPSSD 903
Qy      803 SNDI-----TSIIPSPS-----RPHVNTTSDLSSTFESSSMNTPTSISSDGM 845
Db      904 QSDILTSSTFSTLVVPFSLSSSSSLGTYPHYVNSTTYHASESSSSVASPSMASESAN 963
Qy      846 LLSSTLVTESETTTELICSDGKE---CSRLSSSGIVTN-PDSNESSIVTSTVTPASTM 901
Db      964 --DDTYLTSESTDTTSSIGTDSSTVTFRRDNGDGCIVTGMFSSSIDSGQTSVDTTSSF 1021
Qy      902 SDSLSTG--ISATSSDNV--SKSGVSVTTSTVTTIQTTPNPLSSSVTSLTOLSPSV 958
Db      1022 VASSTFSAEQSLTDPNIDSSQTSASSSTKLVSVDIVVNSISLSETS--TLSSDDST 1079
Qy      959 SESESKVTTSGND---NOSGTHDSQSTSTEIEIVTTS---STKVLPPVSVNNTDLTSE 1011
Db      1080 S-SDTSISSTNSDTCNVNAGSSHTSTASIKESSIQKTGVTLLSSSYLSTKLSTSDITTE 1138
Qy      1012 PTNTRQPTLSTTNSITED---ITTQOP-----TGDNQ-----DNTSSTNPVPT 1054
Db      1139 LIITELITTELITTELITTEDNEPNTFTSPSHSEIFPSDDNSVLKQVDGESTVEIPPV 1198
Qy      1055 VATSTLASAEEDNKGSHESASTSLKPSMGNS-----GLTSTTEAATTSPTA- 1106
Db      1199 TDTTSSSVSVHSTE-----ASTA--TLGENSPKVASAPVNTETSLRSTSSSNHAT 1249
Qy      1107 -----PSPAVSSGT--DVTTEPPTDREOPTLSTTS-KTNSELVATQAT 1148
Db      1250 ESSGTVKSEASAEAIPTPTSTDNRLSYSTEEAKGSTYPNSGSTNNLMTESQVAAPTDST 1309
Qy      1149 N---ENGKSPDLTSSLTGTSTASTSANELAVTS---GSVTGGAVASANDOS--- 1197
Db      1310 SVLTAPVVTSTPDDKSSAAVNPQSKTKSEESIGLSDSVNETNNGFIATLSEAPNSL 1369
Qy      1198 -HSTSVT-----NSNSIVSNTPQTLTSSQVTSVSSPSTNTFTASTYDGSGLIIOH 1245
Db      1370 IHSESISTTMAKTTDASINGDSAAANSQPTTLTQQVATS--SYNQPLITTYAGSSSATKH 1427
Qy      1246 STWLYGLITLLSLF 1259
Db      1428 PSYLLKPFISVALFF 1441

RESULT 5
US-10-245-802-16
; Sequence 16, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
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; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 1270
; TYPE: PRT
; ORGANISM: Candida albicans
; US-10-245-802-16

Query Match      39.8%; Score 2584.5; DB 14; Length 1270;
Best Local Similarity 45.0%; Pred. No. 2.8e-124;
Matches 616; Conservative 195; Mismatches 347; Indels 211; Gaps 37;

Qy 1 MLOQFTLLFLYLISASAKITGVFDPSFNSLTWSNAANYAFKPGYPTWNAVGLWSLDGTS 60
Db 1 MIQFTLLFLYLSPATAKAITGIFNS IDSLTVSNAGNAYFKPGYPTWNAVGLYSLDCTS 60
Qy 61 ANPGDTFLNMPGVKPYKTTTSQTSVDLTADGVKYATCQFYSGEETFTSTLTCTVNDALKS 120
Db 61 ANPGDTFLNMPGVKPYKFTASQKSVDLTADGVKYATCQFYSGEETFTSTLTCTVNDALKS 120
Qy 121 SIKAGTWTLPFAFNVGGTSGSTLEDSKCTAGTNTVTVDNDGDKDISIDVEFEKSTVDP 180
Db 121 SIKAGTWTLPFAFNVGGTSGSTLEDSKCTAGTNTVTVDNDGDKDISIDVEFEKSTVDR 180
Qy 181 SAYLYASRMPSLNKVTLFVAPOCENGYSGTGMFSSNGDVDAIDCSNIHIGITKGLND 240
Db 181 SGYLTTSRFPMLNKIALTYVAPOCENGYSGTGMFSTSYGDVAIDCSNVHIGISKGWVD 240
Qy 241 WNPVSSSFSYTKTCTGNGIQIKQNPAGRPIDAYISATDVNQTYLAYTNDYTCAG 300
Db 241 YNHPVTSESFSYTKSCSFGISITYQNPAGRPIDAYISPSDNNQYLSKYNDYTCVD 300
Qy 301 SRLQSKPTLRTWGVKNSDAGNGIVIVATRTVTDSTAVTTLPPNPSVDKTKTIELQ 360
Db 301 DYQCHAPFTLKYTGKNSDAGNGIVIVATRTVTDSTAVTTLPPNPSVDKTKTIELQ 360
Qy 361 PIPTTIITTSVGVVTSYLTAKTAPIGETATVIDVPYHTTTVTSEWGTGTTTTTRNP 420
Db 361 PIPTTIITTSVGVVTSYLTAKTAPIGETATVIDVPYHTTTVTSEWGTGTTTTTRNP 420
Qy 421 TDSIDTVVQVPLPNPTVSTTEYWSQSFATTTVTAPPGGTDVVIIRPPNHTVTTEYW 480
Db 421 TDSIDTVVQVPLPNPTTTTQFSESEFTSTTTITNKEPGTDSVIVKEPHNPTVTTEFY 480
Qy 481 SQSFATTTVTAPPGTDSVVIIRPPNPTVTTT-----EYWSQSFATTTVT 527
Db 481 SESYATTTTITGPGTDSVVIHDPLESSSTTALESNDISSAQSSSSVEQSSIV 540
Qy 528 APPGGTDSVVIIRPPNPTVTTTEYWSQFATTTVTAPPGGTDVVIIRPPNHTVTTEY 587
Db 541 GLSSSDIPLSDMPS-----SSSTGLTSSESTVSSVSDSSSSSELSFSSSES 591
Qy 588 WSQSFATTTVTAPPGGTDVVIIRPPNHTVTTEYWSQFATTTVTGPGSGTDVVIIR 647
Db 592 YSSSIDSTNPF-----YDSSSDLESTSTITYSSSIDAQSS----- 626
Qy 648 EPPNPTVTTTEYWSQFATTTITAPPG-----TDTVLIIRPPNHTVTTEYWSQF 701
Db 627 -----OSVQSVNSISSTQSTSSGSEENSTVTD-ILVSSDASSILNSD---ISSY 675
Qy 702 TTTTVPAGEDTVLIIRPPNHTVTTEYWSQFATTTVTAPPGGTDVVIIRPPNPT 761
Db 676 PSTTISLSDDPHTI-AGEPDRS-----SSSIASVTEIS-----SDLVSLTSDP--- 719
Qy 762 VTTTEYWSQFATTTVTAPPGGTDVVIIRPPNHTVTTEYWSQFATTTITSPGFS----- 814
Db 720 --TSSPDSSSSLNSDSSSP-----PSDESIDISASSSPSTLVAPSPSLSSSSL 766
```

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Qy 815 ---RPHVNSTTSDLTSTFESSNMNTPTSISSDGMGLLSSTLVTETSETTTLICSDGKE-- 869
Db 767 SLIVPHVNSTTTHASESESSSVASP-SVASESANDDTHL-SESTDTTIIIGTDSSTVT 824
Qy 870 -CSRLSSSGIYV-----NPDSSNESSIVTSTVTASTMSDLSLSDGIGSATSSDNV--SK 921
Db 825 FCRDNGDGCIVTIGTSSSIDSEQTSDVTT---TSSFVASSTPTTSABQSITDNFNIDSSQ 881
Qy 922 SGVSVTTTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSESESKVTFTSNGD-----NOSGT 977
Db 882 TSASSSTKSSVSVDTVVNSILLSETS--TLSSDDGTS-SDTSSISSTNSDTCGINAGSS 938
Qy 978 HDQSSTSTREIIVTTS---STKVLPPVVSNTDLTSEPTWTR-----EOPTTLSSTNS 1028
Db 939 HKSTASIKESSIQKTGVTLSSTLSTKLSSTDIETLITTELTIIEDNEPNTFTSTPSS 998
Qy 1029 ITEDITTSQPTGNG-----DNTSSTNPVPVTATSTLASAREEDKSGSHESASTSLKP 1082
Db 999 HSEIFSS-----DNSVLKSKQVDRSTIKTPTTDTVTVSSLSVHST-----ASTA--- 1044
Qy 1083 SMGENS-----GLTSTSEIATTTTPTAPSPAVSSGT-----DVTTEPTDT--- 1124
Db 1045 TLGENSFNVASTPLNTATSLRSTSSSNHATE---SSGTVKSEASVEAIPSPPTSTDNR 1101
Qy 1125 -----REOPTTLSTTSKTN-----SELVATTQATN---ENGKSPSTDLTSSLTGTSA 1170
Db 1102 LSYSTEEAEGITVANSGSTNNLITESQVAAAPTDTSTSVLIENLVVTSTFDDNSSAAVDQPS 1161
Qy 1171 STSANSRLV---TSGSVTCGAVASANDQSHSTSV-----TNSNSIVS 1210
Db 1162 KTKSIEESIMNPSTNETNNGFIATLSQAQVPSSEIHSELISLTAKTTAKTASMMGDSAA 1221
Qy 1211 NTPOTLTSQVTSSTNTFIASDYSGSIITQHSWLYGLITLLSLF 1259
Db 1222 NSQPTLLIQVATS--SYNQPLITYAGSSATKHPSYLLKPFISVALFF 1268

RESULT 6
US-10-245-802-20
; Sequence 20, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 2297
; TYPE: PRT
; ORGANISM: Candida albicans
; US-10-245-802-20

Query Match      37.8%; Score 2452.5; DB 14; Length 2297;
Best Local Similarity 40.3%; Pred. No. 3.3e-117;
Matches 581; Conservative 234; Mismatches 416; Indels 211; Gaps 24;

Qy 2 LQQTLLFLYLISIAS--AKTITGVFDPSFNSLTWSNAANYAFKPGYPTWNAVGLWSLDGT 59
Db 1 MKKLYLLYLASFTTVISKEVGFNFQNSLIYIYTRARYEEISTLTANAQLEVALDGT 60
Qy 60 SANPGDTFTLNMPCVFKYTTTSQTSVDLTADGVKYATCQFYSGEETFTSTLTCTVNDALK 119
Db 61 IASPGDFTLNMPCVFKYKFTVETSVQLTANSIATCFDAGEDTKPSLSKCTVTDLT 120
Qy 120 SSIKAGTWTLPFAFNVGGTSGSTLEDSKCTAGTNTVTVDNDGDKDISIDVEFEKSTVD 179
Db 121 EDTSVGFSVILPIAFNVGGSGSKSTITDSKCFSSGYNTVTFDGNQNLSTTANFLPRREL 180
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RESULT 8
US-10-245-802-14
; Sequence 14, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-14

Query Match      28.0%; Score 1819; DB 14; Length 469;
Best Local Similarity 72.1%; Pred. No. 1.7e-85;
Matches 338; Conservative 48; Mismatches 83; Indels 0; Gaps 0;

Qy 1 MLOQFTLLFLYLISASAKITGVDFSNLSLWNAANYAFKPGYPTWNAVLSLGDGTS 60
Db 1 MLLQFLLSLCVSATAKVITGVDFSNLSLWNAANYAFKPGYPTWNAVLSLGDGTS 60
Qy 61 ANPGDTFTLNMPCVKYKTSQTSVDLTADGVKATCQFYSGEERTFTSLTCTVNDALKS 120
Db 61 ASAGDTFTLNMPCVKYKTSQTSVDLTADGVKATCQFYSGEERTFTSLTCTVNDALKS 120
Qy 121 SIKAFGTTLPIAFNVGGTSGTDLSDSKCFTAGTNTVTFDNDGDKDISIDVFEKSTVDP 180
Db 121 DTKAIGTTLPIAFNVGGTSGTDLSDSKCFTAGTNTVTFDNDGDKDISIDVFEKSTVDP 180
Qy 181 SAYLYASRVMSPLNKVITLFPVAPCENGYSYTGWTFSSNGDVAIDCSNIHIGITKGLND 240
Db 181 SDRILLSRILPSLQANLFLPQECANGYSYTGWTFSSNGDVAIDCSNIHIGITKGLND 240
Qy 241 WNPVSSSESYTKTCTSNQIYKQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
Db 241 WNPVSSSESYTKTCTSNQIYKQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
Qy 301 SRLQSKPTLAWTKYKNSDAGSNGIVIVATRTVTDSTTAVTTLFPNPSVDKTKTIBILQ 360
Db 301 AASVDDSFTHWGRYSNQSAGSNGITVVTTRVTDSTTAVTTLFPNPSVDKTKTIBILQ 360
Qy 361 PIPTTTITTSYGVVTSYLTAKPIGETATVIVDVPHHTTTTWTSEWGTGTTTTTTRNP 420
Db 361 PIPTTTITTSYGVVTSYLTAKPIGETATVIVDVPHHTTTTWTSEWGTGTTTTTTRNP 420
Qy 421 TDSIDTVVQVPLNPVTSTTEYWSQSFAATTTTVPAGGTDVTIIRREP 469
Db 421 TDSIDTVVQVPLNPVTSTTEYWSQSFAATTTTVPAGGTDVTIIRREP 469

RESULT 9
US-10-245-802-24
; Sequence 24, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
```

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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-245-802-24

Query Match      26.4%; Score 1717.5; DB 14; Length 468;
Best Local Similarity 68.7%; Pred. No. 2.8e-80;
Matches 322; Conservative 69; Mismatches 77; Indels 1; Gaps 1;

Qy 1 MLOQFTLLFLYLISASAKITGVDFSNLSLWNAANYAFKPGYPTWNAVLSLGDGTS 60
Db 1 MLPQFILLFISLWSTAKITGVDFSNLSLWNAANYAFKPGYPTWNAVLSLGDGTS 60
Qy 61 ANPGDTFTLNMPCVKYKTSQTSVDLTADGVKATCQFYSGEERTFTSLTCTVNDALKS 120
Db 61 ADPGDTFTLNMPCVKYKTSQTSVDLTADGVKATCQFYSGEERTFTSLTCTVNDALKS 120
Qy 121 SIKAFGTTLPIAFNVGGTSGTDLSDSKCFTAGTNTVTFDNDGDKDISIDVFEKSTVDP 180
Db 121 YARVSGTTLPIAFNVGGTSGTDLSDSKCFTAGTNTVTFDNDGDKDISIDVFEKSTVDP 180
Qy 181 SAYLYASRVMSPLNKVITLFPVAPCENGYSYTGWTFSSNGDVAIDCSNIHIGITKGLND 240
Db 181 SGVITSSRIIPSLNKLSSLFVWPQCENGYSYTGWTFSSNGDVAIDCSNIHIGITKGLND 240
Qy 241 WNPVSSSESYTKTCTSNQIYKQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
Db 240 YNPVSSSESYTKTCTSNQIYKQNVAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 299
Qy 301 SRLQSKPTLAWTKYKNSDAGSNGIVIVATRTVTDSTTAVTTLFPNPSVDKTKTIBILQ 360
Db 300 GNTVDPFTLTYGYKNSDAGSNGIVIVATRTVTDSTTAVTTLFPNPSVDKTKTIBILQ 359
Qy 361 PIPTTTITTSYGVVTSYLTAKPIGETATVIVDVPHHTTTTWTSEWGTGTTTTTTRNP 420
Db 360 PIPTTTITTSYGVVTSYLTAKPIGETATVIVDVPHHTTTTWTSEWGTGTTTTTTRNP 419
Qy 421 TDSIDTVVQVPLNPVTSTTEYWSQSFAATTTTVPAGGTDVTIIRREP 469
Db 420 TGSIDTVVQVPLNPVTSTTEYWSQSFAATTTTVPAGGTDVTIIRREP 468

RESULT 10
US-09-801-368-104
; Sequence 104, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Bueby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
```


QY 2 LQQTLLFLYLISASAKT-----ITGVDFSF-----NSLTWSNAANYAF----- 40
Db 10 LAVFTLLAL-TSVASGATEACLPAGQRKSGMNIIFYQSLKDSSTYNAAYMAYGYASKT 68
QY 41 -----KPGGYPTW-----NAVLGWSLD--G 58
Db 69 KLGSVGGQTDISIDYINPCVSSSGTFPCQEDSYGNWCKGMGACNSQGIAYWSTDLFG 128
QY 59 TSANPGDFTFLNM-----PCVKYTTSQ-----TSVD 85
Db 129 FYTTFTNV-TLEMTGYFLPQTGSGYTFKFAVDSDAILSVEGATAFNCCAQOQPPISTN 187
QY 86 LTADGVK-----YATCQFSGBEFTFTSLCTVDALKSSIKAFGT-----VTLP 131
Db 188 FTIDGKPMWGSGLPNIEGVYTAGYTPM-----KVVSNAVSGTLPISTVLP 238
QY 132 IAFNVGGTSDLEDKSCFTAGTNTVTFNDGDKDIDIDVEFKSTV-DPSAYLYASRVM 190
Db 239 -----DGTVSDDFEG-----YVVSFDD-----DLQSNCCTVPDPSNYA-VSTTT 277
QY 191 PSLNKKVTLFVAPCENGITSGTMGFSSNGDVAIDCSNIHIGTKGLNDWYVPVSSP 250
Db 278 TTTEPWTGFTSTSTEMTFTVGTNGVPTDETIVIVIRTPPTASTIITTEPMNSTFTST 337
QY 251 SYTKTCTSGIQIKQNVYPAGYRPFIDAYISATDVNQVTLAYNDYTCAGSLQSKPPTL 310
Db 338 ELITVGTNGVKTDETI-----VIRTPPTATTAITTEPMNSTFTSTSEL----- 384
QY 311 RWTGYKSDAGSNGI-----VIVATRTVTDSTAVTTL-PFNPSVDKTKT----- 355
Db 385 -----ITVGTNGLPTDETIIVIRTPPTATTAITTPQWNDTFTSTSTELTFTVGTNGL 438
QY 356 -----IBILOPITPTIIT-----SYGVGTTSYLTKTA-----PGETATVIVDPYH 398
Db 439 PTDETIIVIRTPPTATTAITTPQWNDTFTSTSTELTFTVGTNGLPTDET-IIIVIRTPPT 497
QY 399 TTT-TVTSEWGTIT-----TTTTRN--PTSDIDVVOVPLNPTVSTT-----EY 443
Db 498 ATTAITTPQWNDTFTSTSTELTFTVGTNGLPTD-ETIIIV-IRTPPTATTAITTPQ 552
QY 444 WSQSFAIT-----TIVTAPPG-GTD--TVIIRPPNHT--VTTTEYWSQSFAIT-----TTV 490
Db 553 WNDFTSTSTEMTFTVGTNGLPTDETIIVIRTPPTATTAITTEPMNSTFTSTSTEMTIV 612
QY 491 TAPPG-GTDS--VVIIRPPNHT--VTTTEYWSQSFAIT-----TIVTAPPG-GTDS--VII 538
Db 613 TGTNGLPTDETIIVIRTPPTATTAITTPQWNDTFTSTSTEMTFTVGTNGLPTDETIIV 672
QY 539 REPPNHT--VTTTEYWSQSFAIT-----TIVTAPPG-GTDS--VVIIRPPNHT--VTTTEY 587
Db 673 RTPTATTAITTPQWNDTFTSTSTELTFTVGTNGLPTDETIIVIRTPPTATTAITTPQ 732
QY 588 WSQSFAIT-----TIVTAPPG-GTD--TVIIRPPNHTV--TTEYWSQSFAIT-----TTV 634
Db 733 WNDFTSTSTEMTFTVGTNGLPTDETIIVIRTPPTSEGLISITTEPWTGFTSTSTEMTIV 792
QY 635 T-----GPPSGTDTVIIRPPNHT--VTTTEYWSQSFAIT-----TIVTAP--PGETDTVLI 682
Db 793 TGTNGLPTDETIIVIRTPPTSEGLVTTTTEPWTGFTSTSTEMTFTVGTNGLPTDETIIV 852
QY 683 REPPNHTV--TTEYWSQSFAIT-----TIVTAPPG-GTD--TVIIRPPNHTV--TTEY 731
Db 853 RTPTSEGLISITTEPWTGFTSTSTEMTFTVGTNGLPTDETIIVIRTPPTSEGLISITTEP 912
QY 732 WSQSFAITTTVAPPGTD-----TVIIRPPNHTV--TTEYWSQSFAITTTTIVTAPP 782
Db 913 WGTFTSTSTEMTFTVGTNGLPTDETIIVIRTPPTSEGLISITTEPWTGFTSTSTEMTIV 972
QY 783 GGT-----DTVIIYESMSSSKI-----STGNDITSIIPSFRP----- 816
Db 973 TGTNGLPTDETIIVIRTPPTSEGLISITTEPWTGFTSTSTEMTFTVGTNGLPTDETIIV 1032

QY 817 -----HYNVSTTSD-LSTFESSMMTPTSIISDGMLLSLSTTLVTSETT-----TELICS 865
Db 1033 RPTSEGLVTTTTTEPWTGFTSTSTEMTFTVGTNGLPTDETIIVIRTPPTAIISSSLSSS 1092
QY 866 DGKECRLSSSGIIVNP--DSNESSIVTSTVPTASTMSDLSLSTGIGSATSDNDVSKSG 923
Db 1093 SQGITSITSSRIIT-PFYPNGTSVISSVTSISSVTSLSLFTSSPVISSSVISSSTTTS 1151
QY 924 VSVTTSVTIITQITNPLSSSVTSLTQLSSIPSVSESESKVTFTNGDNQSGTHDSQST 983
Db 1152 TSIFSESSKSSV--IPTSSSTSGSESETSSAGSVSS-----SFISSESKSPYSSSS- 1204
QY 984 STBIVTTSST-----KVLPPVSVSNDLTSBPTNTRPQPTLSTTS-----NSITE 1031
Db 1205 ---LPLVTSATTQETASSLPPATT-----TKTSEQTLVTVTSCSHVCTESISP 1252
QY 1032 DIITSQPTGNGDNTSTN--PVPVTATSLASBEDNKGSHESASTSLKPSMGNSG 1089
Db 1253 AIVSTATVTVSGVTTEYTTWCPISTTETTKQTKGTEQTETTKQITVTVTSSCESDVCS 1312
QY 1090 LTTSTIEATTTGTEAPSPAVSSGTDVTEPTDTRPQPTLSTT-----SKTNSBLV 1142
Db 1313 KTASPAIVSTSTATINGVTTEYTTWCPIST--TESRQQTTLVTVTSCSGVCSSETASPAI 1370
QY 1143 ATT-----QATNNGGKSPSTDLTSSLTGT--SASTSANSSELVTSQSV 1184
Db 1371 VSTATATVNDVTVYPTWRPQTANESVSSKMSATGETTTNTLAETTTNTVAATITN 1430
QY 1185 TGGN-----VASASNDQSHSTSV-----TNSNSIVSNTPTPTLSQ 1220
Db 1431 TGAETKTVVTSLSRSHAEQTASATDVIGHSSSVSVSETGNTKSLTSSGLSTMSQ 1490
QY 1221 VTSSSP-----STNTPIASTYDGSIIQHSWTLYGLITLTLFLI 1260
Db 1491 PRSTPASSVGVYSTASLEISTYAGSANSLLAGSLSVFIASLLAL 1536

RESULT 12

US-10-324-035-17

; Sequence 17, Application US/10324035

; Publication No. US20050084848A1

; GENERAL INFORMATION:

; APPLICANT: Phillips, John

; TITLE OF INVENTION: METHODS OF USING GLUCAN SYNTHASE PATHWAY REPORTER GENES TO SCREEN

; FILE REFERENCE: 9301-178-999

; CURRENT APPLICATION NUMBER: US/10/324,035

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 17

; LENGTH: 1537

; TYPE: PR1

; ORGANISM: Saccharomyces cerevisiae

; US-10-324-035-17

Query Match

Best Local Similarity 14.5%; Score 939; DB 17; Length 1537;

Matches 414; Conservative 246; Mismatches 520; Indels 426; Gaps 84;

QY 2 LQQTLLFLYLISASAKT-----ITGVDFSF-----NSLTWSNAANYAF----- 40
Db 10 LAVFTLLAL-TSVASGATEACLPAGQRKSGMNIIFYQSLKDSSTYNAAYMAYGYASKT 68
QY 41 -----KPGGYPTW-----NAVLGWSLD--G 58
Db 69 KLGSVGGQTDISIDYINPCVSSSGTFPCQEDSYGNWCKGMGACNSQGIAYWSTDLFG 128
QY 59 TSANPGDFTFLNM-----PCVKYTTSQ-----TSVD 85
Db 129 FYTTFTNV-TLEMTGYFLPQTGSGYTFKFAVDSDAILSVEGATAFNCCAQOQPPISTN 187
QY 86 LTADGVK-----YATCQFSGBEFTFTSLCTVDALKSSIKAFGT-----VTLP 131

Db 188 FTIDGKPMGSLPPNIEGTVMYAGYYPM-----KVYVNAVSGTLPISVTLPL 238
Qy 132 IAFNVGGTSGTDLSDSKCTAGTNTVTFNDGDKDISIDVEPEKSTV-DPSAYLYASRV 190
Db 239 -----DGTTVSDDFEG-----YVVSFD-----DLQSNCTVPDPSNYA-VSTTT 277
Qy 191 PSLNKKVTLFVAPOCENGYSGTGMFSSNGDVAIDCSNIHIGITKGLNDWNPVVSSESP 250
Db 278 TTPETWGTST 337
Qy 251 SYTKTCSNGIQIKONVAGYRPFIDAYISATDVNQYTLAYNDYTCAGSRLOKPFLL 310
Db 338 ELTIVTGTNGVRVDETLII-----VIRPTTATTAITTEPWNSTFTSTSTSTSTST 384
Qy 311 RWTGKNSDAGSNGI-----VIVATRTVTDSTTAVTL-PPNPSVDKTKT----- 355
Db 385 -----TIVTGTNGLPTDETLIIIRPTTATTATTAITTPQWNDTFTSTSTSTSTST 438
Qy 356 -----TEILOPIPTTTITT-----SYVGVTTSYLTKTA-----PIGETATVIVDPVYH 398
Db 439 PTDETLIIIRPTTATTATTAITTPQWNDTFTSTSTSTSTSTSTSTSTSTSTSTSTST 497
Qy 399 TTT--TIVSEWGTIT-----TTTTXN--PTDSIDTVVQVPLNPVTSST-----EY 443
Db 498 ATTAMTTQPNWDTFTST 552
Qy 444 WSQSFAAT-----TIVTAPPG-GTD--TVIIREPNNHT--VTTTEYWSQSFAAT-----TTV 490
Db 553 WNDFTST 612
Qy 491 TAPPG-GTDS--VLIIRPPNPT--VTTTEYWSQSFAAT-----TIVTAPPG-GTDS--VII 538
Db 613 TGTNGLPTDETLIIIRPTTATTATTAITTPQWNDTFTSTSTSTSTSTSTSTSTSTST 672
Qy 539 REPPNPT--VTTTEYWSQSFAAT-----TIVTAPPG-GTDS--VLIIRPPNHT--VTTTEY 587
Db 673 RTPTTATTAMTTQPNWDTFTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 732
Qy 588 WSQSFAAT-----TIVTAPPG-GTD--TVIIREPNNHT--VTTTEYWSQSFAAT-----TTV 634
Db 733 WNDFTST 792
Qy 635 T---GPSGTDVLIIRPPNPT--VTTTEYWSQSFAAT-----TTITAP-----PGETDVLII 682
Db 793 TGTNGQPTDETLIIIRPTSEGLVTTTTEPWTGFTSTSTSTSTSTSTSTSTSTSTSTST 852
Qy 683 REPPNHTV--TTPTEYWSQSFAAT-----TIVTAPPG-GTD--TVIIIRPPNHTV--TTPTEY 731
Db 853 RTPTSEGLISTTTEPWTGFTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 912
Qy 732 WSQSFAATTTVTPPGGTD-----TVIIREPNNHTV--TTPTEYWSQSFAATTTVTPAP 782
Db 913 WTGFTST 972
Qy 783 GGT-----DTVIIYESMSSSKI-----STSSNDITSIIPEFSRP----- 816
Db 973 TGTNGQPTDETLIIIRPTSEGLISTTTEPWTGFTSTSTSTSTSTSTSTSTSTSTSTST 1032
Qy 817 -----HYVNSTGSD-LSTFESSNMPTTSISSDGMLLSSTLVSEITT-----TELICS 865
Db 1033 RTPTSEGLVTTTTEPWTGFTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 1092
Qy 866 DGKCSRLLSSSGGLVTPN--DSNESSIVTSTVPTASTMSDLSSTDCISATSSDNVSKSG 923
Db 1093 SQQITSSITSRPIT--PFPYNSGTSVISSSVISSVSSVSSVSSVSSVSSVSSVSSVSS 1151
Qy 924 VSVTTERSVTTIQTTPNPLSSSVTLQLSLIPSVSESKVPTFSGNDNQSGTHDSQST 983
Db 1152 TSIFSESSKSSV--IPTSSSTSGSESESTSSAGSVSS-----SPISSESSKSPYSSSS- 1204
Qy 984 STEIRIVTSTST-----KVLPPVSSNDLTSEPTNTREQPTTLSTTS-----NSITE 1031
Db 1205 ---LPLVTSTSTOETASSLPPATT-----TKTSEQTLTVTVTSCSHVCTESISP 1252

Qy 1032 DITTSOPTGNDGNTSSIN--EVPVATSTLASAEEDNKGSHESASTSLKPSMGENSG 1089
Db 1253 AIVSTATVTVSGVTTEYTWCPISITEITTKQKGTTEQTTKQTTVTVTSSCESDVCS 1312
Qy 1090 LTTSTEIEATTSPTPEAPSPAVSSGTDVTEPTDTRQPTTLSTT-----SKINSELV 1142
Db 1313 KTASPAIVSTATINGVTTEYTWCPIST--TESRQQTLLVTVTSCSGVCSSETASPAI 1370
Qy 1143 ATT-----QATNENGKSPSDTLTSSLTCT--SASTSANGSELVTSGSV 1184
Db 1371 VSTATATVNDVVTVTPWRPOTANESVSSKNSATGETTTNWLAEITNTVAEITIN 1430
Qy 1185 TCGA-----VASASNDQSHSTSV-----TNSNSIVSNTPQTTLSSQ 1220
Db 1431 TGAETKTVVSSLSRSNHAETQTASATDVIGHSSSVSVSETGNTKSLTSSGLSTMSQ 1490
Qy 1221 VTSSSP-----STNTFIASVTYDGGSGIIQHSWTWLYGLITLLSLFI 1260
Db 1491 PRSTPASSVMGYSTASLEISTYAGSANSLLAGSLSVFIASLLAI 1536

RESULT 13

US-09-801-368-114
; Sequence 114, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114
; LENGTH: 1322
; TYPE: PRF
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-114

Query Match 14.4%; Score 932.5; DB 9; Length 1322;
Best Local Similarity 28.1%; Pred. No. 1.8e-39;
Matches 400; Conservative 215; Mismatches 468; Indels 339; Gaps 79;
Qy 28 NSUTWGNAAANYAKPGGYTNAVLGWSLDGTSANPGDFTLNMPCVKYTTISQT----S 83
Db 50 DSSTYGAAYMAY---GYASKT-----KLGSVGGQTDIDYINIPCV---SSSGTFFCPQ 98
Qy 84 VDLTAD-GVK-YATCQ-----PYSCEBFTTPTCTCTVNDALKSSIKAPGTVTLPJA-- 133
Db 99 EDLYGNWKGKIGACSNPIIAYWSDLDLGFYTTPT-----NVTLEMTGY 143
Qy 134 FNVGGTSGSTDLSDSKCTAGTNTVTFNDGDKDISIDVEFEKSTVDPSPAYLYASRVMSPL 193
Db 144 FLPPQTGSYI-----FKPATVDDSAI----- 165
Qy 194 NKVTTFLVAPQCEGNGTSGTMGFSNGDVAIDC-----SNIHIGITKGLNDWN- 242

Db 166 -----SVGSIAPFCAQEQPPITSTNFTI---NGIKPWNG 198
Qy 243 -YPVSSBSFSYTKTCTSGNGIQKQNVPA-GYRPF-----IDAYISATDVN- 286
Db 199 SPPDNIGTVYMYAGFYPMKIVYNAVAMGTLPISVTLPGTTVSDDFEGYVTFNNL 258
Qy 287 ---QYTLAYTNDYTCAGSRLOSKPFTLRWTGYKNSDA-----GSNGI-----VIVATT 331
Db 259 SQPNCTIPDPNSNYTVSTIITTEP-----WTGFTSTSTSTMTVTVGTNGVPTDEIVIVRT 314
Qy 332 RTVDSITAVTTLFPNPSVDKTKIEILQIPPTTIT--TSYGVVTSYLTAKTAPIGETAT 390
Db 315 PT-TASTIITTEPWNSTFTSTST-----ELITVGTNGVTRTDETIIVIRTPPTATTA 366
Qy 391 VIVDPVHTVTTVTSEWGTITTTTTRN--PTDSIDTVVQVPLNPT-VSTTEYWSQS 447
Db 367 ITTTEPWNSTFTSTST---TELTVTGTNGLPTDE-TIIVIRTPPTATTAITTPQWMDT 421
Qy 448 FATT-----TTVTAPP-GTD--TVIIRPPNHT--VTTEYWSQSFAIT-----TTVTAPP 494
Db 422 FTSTSTELTVGTNGLPTDETIIVIRTPPTATTAITTPQWMDTFTSTTELTIVIRTP 481
Qy 495 G-GTDS--VIIRPPNPT--VTTEYWSQSFAIT-----TTVTAPP-GTDS--VIIRPP 542
Db 482 GLPTDETIIVIRTPPTATTAITTPQWMDTFTSTTEITVTGTNGLPTDETIIVIRTP 541
Qy 543 NPT--VTTEYWSQSFAIT-----TTVTAPP-GTDS--VIIRPPNHT--VTTEYWSQS 591
Db 542 TATTAMTTQWMDTFTSTSTMTVTVGTNGLPTDETIIVIRTPPTATTAITTEPWNST 601
Qy 592 YATT-----TTVTAPP-GTD--TVIIRPPNHT--VTTEYWSQSFAIT-----TTVTGP- 637
Db 602 FTSTSTMTVTVGTNGLPTDETIIVIRTPPTATTAITTPQWMDTFTSTSTMTVTVGTN 661
Qy 638 --PSGTDTVIIRPPNPT--VTTEYWSQSFAIT-----TTITAP-----PGETDVTIIRPP 686
Db 662 GLPTDETIIVIRTPPTATTAITTPQWMDTFTSTTEITVTGTNGLPTDETIIVIRTP 721
Qy 687 NPT--VTTEYWSQSFAIT-----TTVTAP-----PGETDVTIIRPPNHTV--VTTEYWSQS 735
Db 722 TATTAMTTQWMDTFTSTSTMTVTVGTNGVPTDETVIVIRTPTESEGLISTTEPMTGT 781
Qy 736 YATT-----TTVTAPP-GTD--TVIIRPPNPT--VTTEYWSQSFAIT-----TTVTAPP 782
Db 782 FTSTSTMTVTVGTNGVPTDETVIVIRTPTESEGLVTTTEPMTGTFTSTSTMTVTVGTN 841
Qy 783 G-GTDTVIIRPPNPT--VTTEYWSQSFAIT-----FSRPHYVNSTTDLSTPSSSM 834
Db 842 QOPTDETVIIRTPPTATTAITSSLSGSGQITSPITSARPIITFPYPSNGTSVSSSVISS 901
Qy 835 NPTISSDGM---LLSSTLVTESETTELICSGKCSRLLSSSGIVTAPDSSNESSIV 891
Db 902 DTSLSVSSSVTSLVTSPPVSSSFSSPVSSTTSASILSSS-----K 948
Qy 892 TSVTPTASTMDSLSLSTGIGSATSDNVSKSVSTTSTSTVTTIITPNPLSSSVTSLTQ 951
Db 949 SSVIPTSSTSGSESETSGSASSAS---SSSSISSESPKSTYSSSSLP-PVTSATTSOEI 1004
Qy 952 LSSIPSVSSESKVFTNSGDNQSGTHDSQSTSTIEIVTSSSTKVLPPVWSSNDLASE 1011
Db 1005 TSSLPVPVTTKT-----SQDTLVTVTSCESHVCTESISSAIVSTAT 1046
Qy 1012 PT---NTRQOPTTLTSTNSITEDIT--TSQPTGDNQDNSTSNPVTATSTLASASED 1067
Db 1047 VTVSGATTEYTWCPISITTEIKQTTEIKQKGTTEQTTETTKQTVVT---ISSCESD 1103
Qy 1068 --NKSGSHESASTSLKPSMGENSEGLTSTTEIETATTSPEARSPAVSGTDVTTTEPTDR 1125
Db 1104 VCSKTASPAIVSTSTATINGVTVTYTTCPISTTESKQQTLLVTVTSCGSGVCSETT--- 1160
Qy 1126 EQPTTLSTTKTNSSELVAT-----TQATWNGKSPSTDLTSLTGTTSAST-----SA 1174

Db 1161 -SPAIVSTATATVNDVVTVSTWRPOTTNEQSVSSKMSNSATSETTNTNGAAETTTSTGAA 1219
Qy 1175 NSBLVTSGSVT-----GGAVASASNQSHSTSV-----TMSNSIVSNPTQTLTSSQVTVSS 1224
Db 1220 ETKTVTVTSSISRFNHAETQTASATDVIGHSSVVSVSETGNTKSLTSSGLSTMSQQPRST 1279
Qy 1225 -----SPSTNTFIATYDQSGSIHQSHSTWLYGLITLLSLFI 1260
Db 1280 PASSMWGSSTASLEISTYAGSANSLLAGSLGVFIASLLALAI 1321
RESULT 14
US-10-369-493-1353
; Sequence 1353, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1353
; LENGTH: 1322
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1353

Query Match 14.4%; Score 932.5; DB 15; Length 1322;
Best Local Similarity 28.1%; Pred. No. 1.8e-39;
Matches 400; Conservative 215; Mismatches 468; Indels 339; Gaps 79;
Qy 28 NSLTWNAANVAPKPGVPTWNAVLGWSLDSGTANSAPGDTFTLNNPCVFKYTTSTQ-----S 83
Db 50 DSSITSNAYWAY---GYASKT-----KLSGVGGQTDISIDYINPCV---SSSGTFFPCPQ 98
Qy 84 VDLTAD-GVK-YATCQ-----FYSGBEFTTFTLTCTVNDALKSSIKAFOTVTLPIA-- 133
Db 99 EDLYGNWCKGIGACSNPPIAYWSTDLFGYTTPT-----NVLTLEMTGY 143
Qy 134 FNVGGTSGSTLDESCKFTAGTNTVTFNDGDKDISIDVEPEKSTVDPSAIVLYASRVMSL 193
Db 144 FLPPQTGSYT-----FKPATVDDSAI----- 165
Qy 194 NKVTTLFVAPCENGYSYTGTFSSNGDVAIDC-----SNHIGITKGLNDWN- 242
Db 166 -----SVGSIAPFCAQEQPPITSTNFTI---NGIKPWNG 198
Qy 243 -YPVSSBSFSYTKTCTSGNGIQKQNVPA-GYRPF-----IDAYISATDVN- 286
Db 199 SPPDNIGTVYMYAGFYPMKIVYNAVAMGTLPISVTLPGTTVSDDFEGYVTFNNL 258
Qy 287 ---QYTLAYTNDYTCAGSRLOSKPFTLRWTGYKNSDA-----GSNGI-----VIVATT 331
Db 259 SQPNCTIPDPNSNYTVSTIITTEP-----WTGFTSTSTSTMTVTVGTNGVPTDETVIVRT 314
Qy 332 RTVDSITAVTTLFPNPSVDKTKIEILQIPPTTIT--TSYGVVTSYLTAKTAPIGETAT 390
Db 315 PT-TASTIITTEPWNSTFTSTST-----ELITVGTNGVTRTDETIIVIRTPPTATTA 366
Qy 391 VIVDPVHTVTTVTSEWGTITTTTTRN--PTDSIDTVVQVPLNPT-VSTTEYWSQS 447
Db 367 ITTTEPWNSTFTSTST---TELTVTGTNGLPTDE-TIIVIRTPPTATTAITTPQWMDT 421
Qy 448 FATT-----TTVTAPP-GTD--TVIIRPPNHT--VTTEYWSQSFAIT-----TTVTAPP 494

Db 422 FTSTSTBLTAVTGTNGLPDDETIIVIRTPATTATTAMTTTQPMNDTFTSTSTELTAVTGTN 481
Qy 495 G-GTDS--VLIIRPPNPT--VTTTEYWSQSFAIT---TTVTAPPG-GTDS--VLIIRPP 542
Db 482 GLPDETIIVIRTPATTATTAMTTTQPMNDTFTSTSTELTAVTGTNGLPDTDETIIVIRTP 541
Qy 543 NPT--VTTTEYWSQSFAIT---TTVTAPPG-GTDS--VLIIRPPNHT--VTTTEYWSQS 591
Db 542 TATTAMTTTQPMNDTFTSTSTEMTTVTGTNGLPDDETIIVIRTPATTATTATTTPEWNST 601
Qy 592 YATT---TTVTAPPG-GTD--VLIIRPPNHT--VTTTEYWSQSFAIT---TTVTGP- 637
Db 602 FTSTSTEMTTVTGTNGLPDDETIIVIRTPATTATTATTTQPMNDTFTSTSTEMTTVTGTN 661
Qy 638 --PSGTDVLIIRPPNPT--VTTTEYWSQSFAIT---TTITAP--PGETDVLIREPP 686
Db 662 GLPDETIIVIRTPATTATTAMTTTQPMNDTFTSTSTELTAVTGTNGLPDTDETIIVIRTP 721
Qy 687 NHT--VTTTEYWSQSFAIT---TTVTAP---PGETDVLIREPPNHTV--VTTTEYWSQS 735
Db 722 TATTAMTTTQPMNDTFTSTSTEMTTVTGTNGVPDDETIIVIRTPTEGLISITTEPWGT 781
Qy 736 YATT---TTVTAPPG-GTD--VLIIRPPNPT--VTTTEYWSQSFAIT---TTVTAPP 782
Db 782 FTSTSTEMTTVTGTNGQPDDETIIVIRTPTEGLVTTTTEPWGTFTSTSTEMTTITGTN 841
Qy 783 G-GTDTVLIIRPPNPT--VTTTEYWSQSFAIT---PSRPHVNSSTSDLTPESSSM 834
Db 842 GQPDDETIIVIRTPATTATTSLSSSSGQITFTSARPIITPPYPSNGTSVSISSVSS 901
Qy 835 NPTSTSSGDM--LISSTLVTESETTTELIICSDGKCEKSRSSSGIIVTNPDNESSIV 891
Db 902 DTSSLVSSSVTSLVTSPISSPFISSPVISSVTSISILSESS-----X 948
Qy 892 TSVPTASTWDSLSSTPDGTSATSSDNVSGSVVTEVTSVTIQTTPNPLSSSVTLQ 951
Db 949 SSVIPTSSTSGSESETGASGAS--SSSSISSESPKSTYSSSLIP-PVTSATTSQEI 1004
Qy 952 LSIIPVSESESKVFTPSNGDNQSGHDSQSTTEIIVTSSTKVLPPVVSNTDLTSE 1011
Db 1005 TSSLPPVTTTKT-----SEQTLLVTVTSCHSVCTESISSAIVSTAT 1046
Qy 1012 PT---NREOPTLSTTSNSITEDIT-TSOPTGNDGNTSSTNPVPTVATSTLASASEED 1067
Db 1047 VTVSGATTEYTWCPISITTEITKQTTETTKQTKTEQTTETTKQTTVVT---ISSCED 1103
Qy 1068 --NKGSHGESASTLKPMSGENGLTTSIEIATTSPTAPSPAVSSGTDVTEPTDTR 1125
Db 1104 VCSKTASPAIVSTSTATINGVTEYTWCPISITTESKQQTLLVTVTSCHSVCTESISSAIVSTAT 1160
Qy 1126 EQPTLSTSTKTNSELVAT---TOATNENGKSPSTDLTSSLTGTSAST-----SA 1174
Db 1161 -SPAIVSTATVNDVVTVVTSWRPQNTNEQSVSSKRNNSAISTETNTGAEATTTSTGAA 1219
Qy 1175 NSELVTSQSVT---GGAVASASNDQSHSTSV-----TNSNSIVSNTPOTLLSQQVTS 1224
Db 1220 ETKTVTSSISRNHARTQASATDVIGHSSVVSVSETGNTKSLSSGLSTWSQPRST 1279
Qy 1225 -----SPSTNVTFIASDYGSGSIHQHSWLYGLITLLSLFI 1260
Db 1280 PASSMWGSSTASLEISTYAGSANSLLAGSLGVFIASLLALAI 1321

RESULT 15

US-09-922-217-1068
; Sequence 1068, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy

; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1068
; LENGTH: 5179
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-922-217-1068

Query Match 11.1%; Score 721.5; DB 9; Length 5179;
Best Local Similarity 25.3%; Pred. No. 6e-28;
Matches 335; Conservative 158; Mismatches 554; Indels 279; Gaps 54;

Qy 59 TSANPGDFTLAMPVCFKYTTTSQTSVDLTADGKYKATCOFYSGEEFTTSTLTCTVNDAL 118
Db 1647 TTTTTPPTTTPSP-----TTTTPSPPITTTTTTPPTT-----TPSSPITTPSPPT 1693
Qy 119 KSIIKAFGVTVPIARNVCGTSSDLESKCTAGTNTVNDGDKDISIDVEPKSTV 178
Db 1694 TMTTTPSPPTTTPSPPTTTTTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTT 1747
Qy 179 DP---SAYIVASRVMSLNKVT-----TLFVAPQCE-NGY-TSGTGFSSSSNGDVA 224
Db 1748 PTTTSSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTTTPSPPTT 1807
Qy 225 IDCSNIHIGITKGLDNWYFVSSEFSY-----TKTC-TSNGIQIKYQN-VPAGY 272
Db 1808 L-----IGDVCG-PCGAANISCRATMYPDPVPIGQLGQTVCDVSVGLICKNEDQKPGV 1860
Qy 273 RPIDAYISATDVNQVTLAYNDYTCAGSLRSKPTLRTWTKYKNSDASNGIIVATIR 332
Db 1861 IPW-----AFCLNYEINVQCC--ECVTQPTTMTTNTTENFTPTTPTTPTTPTTPTT 1907
Qy 333 TVTDSFTAVTLPENPSVDKTKTIELQIPITTIITSYVGVTSYLTKTAPIG-ETATV 391
Db 1908 TPTPTGTGTPT 1967
Qy 392 IVDPVYHTTTTVTSEWGT-----TTTTT-----TRTNPTDSIDTVVQVP 432
Db 1968 ---TPITTTTPT 2024
Qy 433 LNPPTVSTTEYWSQSFAITTTTAPPGTDVLIIRPPNHTVTTTEYWSQSFAITTTTVA 492
Db 2025 TETPTGTQTP-TTPTPTTTTPTPTPTPTGT---QPTTPTPTT-----TTVTPPT 2072
Qy 493 PPGTD-----SVLIIRPPNPTVTTTEYWSQSFAITTTTAP-----PGTD-----S 535
Db 2073 TPTGTQPT 2132
Qy 536 VLIIRPPNPTVTTTEYWSQSFAITTTTAP-----PGTDSVLIIRPPNHTVTTTEYWSQS 592
Db 2133 TTTTPT 2180
Qy 593 ATTTTAPPGTDVLIIRPPNHTVTTTEYWSQSFAITTTTVPSPSGTD-----T 643
Db 2181 -TTVPTPTPTGTGT-----PTTPTPTT-----TTVPTPTPTGTPTPTPTPTPT 2226
Qy 644 VLIIRPPNPTVTTTEYWSQSFAITTTTAPPGTDVLIIRPPNHTVTTTEYWSQSFAIT 703
Db 2227 TTVPTPTPTGTGTPT-TTPTPTTTTPTPTPTPTGT-----QPTPTT-----PTTPT 2272
Qy 704 TTVTAPPGTDVLIIRPPNHTVTTTEYWSQSFAITTTTVPAPGGTD-----TVII 754

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